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96007

From: Slobodyansky, Elizabeth
Sent: Friday, June 06, 2003 11:35 AM
To: STIC-Biotech/ChemLib
Subject: 09/800,187

Please search for case 09/800,187:

ED

SEQ ID NOs: 5 and 6 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

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CREE

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Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 6/16/03
Date Completed: 6/16/03
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 03/02
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 14:52:03 ; Search time 53 Seconds
(without alignments)
3054.708 Million cell updates/sec

Title: US-09-800-187-6

Perfect score: 6397

Sequence: 1 MISTGDSITTTTQRKRSRQNP.....LDVKINIAHQNKFGEDMPHPH 1215

Scoring table:

BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq.101002.*
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21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
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23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6397	100.0	1215	23	AAE22856 Human histone deac
2	6364	99.5	1215	23	AAU99661 Human histone deac
3	4022	62.9	817	22	AAU95640 Human histone deac
4	3816	59.7	726	22	AAU93058 Human histone deac
5	1810	28.3	883	22	AAU93058 Human histone deac
6	1749.5	27.3	363	22	AAU00244 Drosophila melanog
7	1132	17.7	675	21	AAU42743 Human histone deac
8	1129.5	17.7	686	21	AAU42757 Human histone deac
9	1127.5	17.6	662	23	AAU81614 Human HDAC9 varian
10	1125	17.6	673	23	AAU81613 Human HDAC9 protei

11	1125	17.6	673	23	AAE22854	Human histone deac
12	970	15.2	625	23	AAU81615	Human HDAC9 varian
13	895	14.0	330	22	AAU23410	Novel human enzyme
14	805.5	12.6	967	22	AAU95659	Human histone deac
15	801.5	12.5	967	22	AAU95659	Human histone deac
16	783.5	12.2	614	22	AAU92700	Human histone deac
17	782.5	12.2	1008	22	AAU78891	Human histone deac
18	782.5	12.2	1020	22	AAU78891	Human histone deac
19	779.5	12.2	574	22	AAU79875	Human histone deac
20	778.5	12.2	716	22	AAU97032	Human histone deac
21	778.5	12.2	1141	21	AAU43008	Human histone deac
22	767.5	12.0	717	23	AAU99660	Human histone deac
23	762.5	11.9	597	20	AAU07092	Human histone deac
24	758.5	11.9	541	21	AAU42845	Human histone deac
25	757.5	11.8	1235	22	AAU58493	Human histone deac
26	755.5	11.8	855	23	AAU99662	Human histone deac
27	730	11.4	425	23	AAU89750	Human histone deac
28	729.5	11.4	1428	21	AAU97033	Human histone deac
29	724.5	11.3	552	21	AAU51590	Human histone deac
30	722	11.3	468	21	AAU51592	Human histone deac
31	722	11.3	499	21	AAU51591	Human histone deac
32	716.5	11.2	532	21	AAU09530	Human histone deac
33	714	11.2	468	21	AAU09532	Human histone deac
34	714	11.2	499	21	AAU09531	Human histone deac
35	694.5	10.9	328	21	AAU45473	Human histone deac
36	659	10.3	327	21	AAU45474	Human histone deac
37	588	9.2	276	22	AAU92577	Human histone deac
38	533	8.3	100	21	AAU39056	Human histone deac
39	517	8.3	398	21	AAU07246	Human histone deac
40	410	6.4	377	21	AAU07247	Human histone deac
41	409.5	6.4	334	22	AAU96309	Human histone deac
42	408	6.4	335	20	AAU07248	Human histone deac
43	390	6.1	335	20	AAU97110	Human histone deac
44	298.5	4.7	301	22	AAU67811	Human histone deac
45	298.5	4.7	501	22	AAU67165	Human histone deac

ALIGNMENTS

RESULT 1	
AAE22856	
ID	AAE22856 standard; Protein: 1215 AA.
XX	
AC	AAE22856;
XX	
DT	21-AUG-2002 (first entry)
XX	
DE	Human histone deacetylase 6 protein.
XX	
KW	Human: histone deacetylase 6; therapy: cancer; bait protein; cytosolic;
KW	enzyme.
XX	
OS	Homo sapiens.
XX	
PN	W0200230970-A2.
XX	
PD	18-APR-2002.
XX	
PF	11-OCT-2001; 2001MO-EP11759.
XX	
PR	13-OCT-2000; 2000US-239928P.
XX	
PA	(FARB) BAYER AG.
XX	
PI	Zhu Z;
XX	
DR	WPI; 2002-416859/44.
XX	
PT	New human histone deacetylase polypeptide useful for identifying
PT	modulating agents that can be used for treating diseases such as cancer
XX	

ps Dislosure; fig 4; 116pp; English.

xx The present invention relates to novel histone deacetylase proteins and
 CC polynucleotides encoding them. Sequences of the invention are useful for
 CC identifying modulating agents that are used for preventing, ameliorating,
 CC treating or correcting dysfunctions or diseases such as cancer. They can
 CC also be used to screen for human histone deacetylase activators and
 CC inhibitors. They are useful for generating antibodies and can be used as
 CC bait proteins in two-hybrid assay or three-hybrid assay. The present
 CC sequence is human histone deacetylase 6 protein.

xx Sequence 1215 AA;

Query Match 100.0%; Score 6397; DB 23; Length 1215;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MTSTGQDSTTRQRRSRQNPQSPQDSSVTSKRNIKKGAVPKRSIPPLAEVKKKKKKKKG 60
DB 1 MTSTGQDSTTRQRRSRQNPQSPQDSSVTSKRNIKKGAVPKRSIPPLAEVKKKKKKKKG 60
OY 61 QAMEEDLIVGLOGMDLNEAEALAGTGLVLDQLEFHCIMDSEPEGEPLAIKEOLI 120
DB 61 QAMEEDLIVGLOGMDLNEAEALAGTGLVLDQLEFHCIMDSEPEGEPLAIKEOLI 120
OY 121 QEGILDRCVSPQARAEKEELMLVHSLEYIDMETTQYNNEGELRYLATYDSVYLHPNS 180
DB 121 QEGILDRCVSPQARAEKEELMLVHSLEYIDMETTQYNNEGELRYLATYDSVYLHPNS 180
OY 181 YSCACLAGSGVRLVDVAGAEIRNGMATIRPPGHHAQSLMDGYCMFNHVAARYAQO 240
DB 181 YSCACLAGSGVRLVDVAGAEIRNGMATIRPPGHHAQSLMDGYCMFNHVAARYAQO 240
OY 181 YSCACLAGSGVRLVDVAGAEIRNGMATIRPPGHHAQSLMDGYCMFNHVAARYAQO 240
DB 181 YSCACLAGSGVRLVDVAGAEIRNGMATIRPPGHHAQSLMDGYCMFNHVAARYAQO 240
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DB 241 KHRIRKRVILVDMVHHGGTQFTPDQDSVLYFSIHRREQGRFWPLKASNNSTGEGOG 300
OY 241 KHRIRKRVILVDMVHHGGTQFTPDQDSVLYFSIHRREQGRFWPLKASNNSTGEGOG 300
DB 241 KHRIRKRVILVDMVHHGGTQFTPDQDSVLYFSIHRREQGRFWPLKASNNSTGEGOG 300
OY 301 QGYTINVMNNOVGMDADYIAAFVHLVPLALEPQOLVLAAGPDALOGDKGEMAAP 360
DB 301 QGYTINVMNNOVGMDADYIAAFVHLVPLALEPQOLVLAAGPDALOGDKGEMAAP 360
OY 301 QGYTINVMNNOVGMDADYIAAFVHLVPLALEPQOLVLAAGPDALOGDKGEMAAP 360
DB 301 QGYTINVMNNOVGMDADYIAAFVHLVPLALEPQOLVLAAGPDALOGDKGEMAAP 360
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DB 361 AGFALQTLHLMLAGLCKLILSLGGYNLRALAEVGSASLHTLGLDPCPMLSEPGAPCRSA 420
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DB 361 AGFALQTLHLMLAGLCKLILSLGGYNLRALAEVGSASLHTLGLDPCPMLSEPGAPCRSA 420
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DB 421 QASVSCALELEPEFVEVLVSTETIVERDMEEDNVEESEEGPWEPPVPLILTWPYLQSR 480
OY 421 QASVSCALELEPEFVEVLVSTETIVERDMEEDNVEESEEGPWEPPVPLILTWPYLQSR 480
DB 421 QASVSCALELEPEFVEVLVSTETIVERDMEEDNVEESEEGPWEPPVPLILTWPYLQSR 480
OY 481 TGLVYDMMNMHNCNMDSHHPVPRILRLIMCRLEELIAGACILTLTPRPAEALITLCH 540
DB 481 TGLVYDMMNMHNCNMDSHHPVPRILRLIMCRLEELIAGACILTLTPRPAEALITLCH 540
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DB 481 TGLVYDMMNMHNCNMDSHHPVPRILRLIMCRLEELIAGACILTLTPRPAEALITLCH 540
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DB 541 SAEVGHILRATEKMTRELHRESSNFDSTIYICPSTFACQLATGAACRLVEAVLSEEVN 600
OY 541 SAEVGHILRATEKMTRELHRESSNFDSTIYICPSTFACQLATGAACRLVEAVLSEEVN 600
DB 541 SAEVGHILRATEKMTRELHRESSNFDSTIYICPSTFACQLATGAACRLVEAVLSEEVN 600
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DB 601 GAAVVRPFGHAEODACGCFEFSNVAVAARHAQITSGHALRLILVDMVHHGNGTOHMF 660
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DB 661 EDDPSVLVSLHRYHGTFFPMGDGASQIGRAAGTGTVVAVANGPMGADYLAAMH 720
OY 661 EDDPSVLVSLHRYHGTFFPMGDGASQIGRAAGTGTVVAVANGPMGADYLAAMH 720
DB 661 EDDPSVLVSLHRYHGTFFPMGDGASQIGRAAGTGTVVAVANGPMGADYLAAMH 720
OY 721 RLVLPIAEFNPDELVSAGFPAAGDPLGGCVSPREGAHLTHLLMLGASRIILILEG 780
DB 721 RLVLPIAEFNPDELVSAGFPAAGDPLGGCVSPREGAHLTHLLMLGASRIILILEG 780
OY 721 RLVLPIAEFNPDELVSAGFPAAGDPLGGCVSPREGAHLTHLLMLGASRIILILEG 780
DB 721 RLVLPIAEFNPDELVSAGFPAAGDPLGGCVSPREGAHLTHLLMLGASRIILILEG 780
OY 781 GYNLTISSESMAACTRSLGDPPPLTLPRPLSGALASTETIGVHRRYRSLRYMKVE 840
DB 781 GYNLTISSESMAACTRSLGDPPPLTLPRPLSGALASTETIGVHRRYRSLRYMKVE 840

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OY 841 DREGSSSKLYTKKAPQAPKPRLAERNTREKRYLPAKMGKNTYSASGEESTPGQTNSET 900
DB 841 DREGSSSKLYTKKAPQAPKPRLAERNTREKRYLPAKMGKNTYSASGEESTPGQTNSET 900
OY 901 AVVALRQDPPSEATGATLAOTISPAIGAMIGOTTSEAVAGATPDOTTSEETVGA 960
DB 901 AVVALRQDPPSEATGATLAOTISPAIGAMIGOTTSEAVAGATPDOTTSEETVGA 960
OY 961 ILDQTTSEDAVGATLGOTTSEAVAGATLAOTISEAMGATLDOTTSEAPGTBLIQ 1020
DB 961 ILDQTTSEDAVGATLGOTTSEAVAGATLAOTISEAMGATLDOTTSEAPGTBLIQ 1020
OY 1021 TPLASTDQTPPTSPVQGTTPDISPSTLIGSRITLSESGSASQAPGENILGEA 1080
DB 1021 TPLASTDQTPPTSPVQGTTPDISPSTLIGSRITLSESGSASQAPGENILGEA 1080
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DB 1081 AGGDMADSMKMGSGGLTFOALFYAVTPPLPCKPHLVAVCPPIPAAGLDVTPCGDCGTIQ 1140
OY 1141 ENMVCLSCYQVYCGRYINGHMLQHGNSGHPLVLSYIDLSAMCYCCQAYVHHQALDVK 1200
DB 1141 ENMVCLSCYQVYCGRYINGHMLQHGNSGHPLVLSYIDLSAMCYCCQAYVHHQALDVK 1200
OY 1201 IAHONKFGEDMPHPH 1215
DB 1201 IAHONKFGEDMPHPH 1215

RESULT 2
AAU99661
ID AAU99661 standard; protein; 1215 AA.
XX
XX AAU99661;
AC
XX
XX 07-OCT-2002 (first entry)
DE
XX Human histone deacetylase isoform 6.
XX
XX Human; histone deacetylase; HDAC-6; cancer; cytostatic;
KW antisenese; tumour suppressor; cell proliferation; tumour;
XX programmed cell death; necrotic cell death.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH
FH Misc-difference 171
FT
FT Misc-difference 244
FT
FT Misc-difference 334
FT
FT Misc-difference 388
FT
FT Misc-difference 410
FT
FT Misc-difference 474
FT
FT Misc-difference 512
FT
FT Misc-difference 519
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FT Misc-difference 526
FT
FT Misc-difference 581
FT
FT Misc-difference 594
FT
FT Misc-difference 599
FT
FT Misc-difference 621

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OY 1201 IAHQNKFGEDMPHP 1215
DB 1201 IAHQNKFGEDMPHP 1215

RESULT 3
AAB95640
ID AAB95640 standard; Protein; 817 AA.

AC AAB95640;
XX 26-JUN-2001 (first entry)
XX Human protein sequence SEQ ID NO:18380.
DE Human protein sequence SEQ ID NO:18380.
XX Human; primer: detection; diagnosis; antisense therapy; gene therapy.
KW Homo sapiens.

OS Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-0116126.
XX 29-JUL-1999; 99JP-0248036.
XX 27-AUG-1999; 99JP-0300253.
XX 11-JAN-2000; 2000JP-0118776.
XX 02-MAY-2000; 2000JP-0183767.
XX 09-JUN-2000; 2000JP-0241899.

PA (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
DR WPI: 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT full-length cDNAs of the abnormality of the proteins encoded by the
PT full-length cDNAs -
PS Claim 8; SEQ ID 18380; 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
XX AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.

Sequence 817 AA;

Query Match 62.98; Score 4022; DB 22; Length 817;
Best Local Similarity 99.38; Pred. No. 3.8e-312;
Matches 758; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MSTGQDSTTTTTRRSRONFQSPDSSVSKRIKKGAVPRISIPNLAEVKKKKMKKLG 60
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OY 61 QAMEEDLIVGLQGMNDLNEALAGTGLVLEQOLNEFHCLMDSPFGPRLHAIKBOLI 120
DB 61 QAMEEDLIVGLQGMNDLNEALAGTGLVLEQOLNEFHCLMDSPFGPRLHAIKBOLI 120
OY 121 QEGILDRCVSFQARFAKEKELMIVHSLEYIDMETTOYANMGEIRVADYDYSYLLPNS 180
DB 121 QEGILDRCVSFQARFAKEKELMIVHSLEYIDMETTOYANMGEIRVADYDYSYLLPNS 180
OY 181 YSCACLASGSVLRVDAVLAETIRNGMALTIRPGHHAQHSIMDGYCFNHVAARYAQ 240
DB 181 YSCACLASGSVLRVDAVLAETIRNGMALTIRPGHHAQHSIMDGYCFNHVAARYAQ 240
OY 241 KHRIRRVLIYDWDVHHGGQTQFTFDQPSVLYFSIRHYEGRFPPLIKASNMSTGFGQG 300
DB 241 KHRIRRVLIYDWDVHHGGQTQFTFDQPSVLYFSIRHYEGRFPPLIKASNMSTGFGQG 300
OY 301 QGTTIVPMNOVMKRDADYIAAFLVLLPALFQOLVVAAGFALQDPPKEMATP 360
DB 301 QGTTIVPMNOVMKRDADYIAAFLVLLPALFQOLVVAAGFALQDPPKEMATP 360
OY 361 AGPAQLTHLMGLAGKLTILLEGYVLRALAGVSASLTLLDPCPMLESPPACPRSA 420
DB 361 AGPAQLTHLMGLAGKLTILLEGYVLRALAGVSASLTLLDPCPMLESPPACPRSA 420
OY 421 QASVSCALEALPEFWEVLVSTETVERDNNEEDNVESEEGPEVPVLLTPVLIQSR 480
DB 421 QASVSCALEALPEFWEVLVSTETVERDNNEEDNVESEEGPEVPVLLTPVLIQSR 480
OY 481 TGLVYQONNMNHNNDSDHPEVPORTLRIMCRLEELGLGRCLTTPRRTAEELTCH 540
DB 481 TGLVYQONNMNHNNDSDHPEVPORTLRIMCRLEELGLGRCLTTPRRTAEELTCH 540
OY 541 SAEYVGLHRTAEKMKTRRELHRESSNEDSIYICSTFCAQLATGAACRLVEAVLSEVLN 600
DB 541 SAEYVGLHRTAEKMKTRRELHRESSNEDSIYICSTFCAQLATGAACRLVEAVLSEVLN 600
OY 601 GAAVVRPFGHHAQDAACGCFPNVSAVAARHAQTISGHALRILIVMDVHHNGTQHF 660
DB 601 GAAVVRPFGHHAQDAACGCFPNVSAVAARHAQTISGHALRILIVMDVHHNGTQHF 660
OY 661 EDDPSVLYVSLAHVYDGTFFPMGDEGASSQIGRAAGCFVNVAMNCPBMGDADYLAWH 720
DB 661 EDDPSVLYVSLAHVYDGTFFPMGDEGASSQIGRAAGCFVNVAMNCPBMGDADYLAWH 720
OY 721 RLVLPIAYEPNPELVVYASGFDAAAGDPLGCGCVSPGVAHLT 763
DB 721 RLVLPIAYEPNPELVVYASGFDAAAGDPLGCGCVSPGVAHLT 763

RESULT 4
AAB93058
ID AAB93058 standard; Protein; 726 AA.

AC AAB93058;
XX 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:11864.

XX Human; primer: detection; diagnosis; antisense therapy; gene therapy.

OS Homo sapiens.

Sequence EP1074617-A2.

cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB116176-AB130511), expressed DNA sequences (AB101840-AB116175) and the encoded proteins (AB17737-AB172072).
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_sequences.

XX Sequence 883 AA;

Query Match 28.3%; Score 1810; DB 22; Length 883;
 Best Local Similarity 46.7%; Pred. No. 2.7e-135;

Matches 371; Conservative 135; Mismatches 237; Indels 52; Gaps 17;

86 TGLVLEDOLENEFCLMDSPFEPGERLHAKEQLIOGLIDRCVSEFOARFEKEELVH 145
 31 TALIYDESMOHCCLMDKEHECEPERFTRVLERCRELNLTERLEPSRSATNDELIRH 90
 146 SLEFYD-LMETTYOYNEGELRVADTYDSYLLHPNSTSCACLAGSVLRVDAVLGAER 204
 91 TEHEFERLKETSGIRDERMEELSSRYDSIYIHPSTFELSLASGSTIELVDHLVAGKQ 150
 205 NGMAIIRPGHNAHSHLMDGYCMENHVAAYAAQOKHRIIRVLLIYDMVDVHHGQGTFF 264
 151 NGMAIIRPGHNAHMAKAEYNGICEFNVALATQHALDVHKLQRLILIDYVHHGQGTFF 210
 265 DDDPSVLYSESIRHYEGRFPHLKASNMSTTGGGOGYTTINPMNOVGKRDADYIAFL 324
 211 YMDPRVYVESIRHFEHSGFMPHLHESDYHAISGAGGYNFNPVLAATGMTNDYLAIFQ 270
 325 HTLLPALFEPOLVYVAAGFDALQDPPKEMATPAGFQOLTHLMGLAGKLLISLEG 384
 271 QLLLPALFEPOLVYVAAGFDALQDPPKEMATPAGFQOLTHLMGLAGKLLISLEG 330
 385 GYNLRALAGVSASLTLLGDPC-PMLESPGAP-CSSAOSVSCALELPEFVEVL-VRS 441
 331 GYCLDSLAGCALTLTSLGLDPCPLVEYTPPLRAELQALLSC-IAYHNPWRCLQLOQ 389
 442 T-----ETVERDNKED-NVESESEEGPMPRPV-----LPI-----LT-----WPVL 477
 390 TDCVELQDRDK-EEDLHTVLRHMIGSP-PRMDRYPTROTALPLPERKLTISNAARQVL 446
 478 GSRGTG-----YTDQNMAMHCLMDSHNRPVQRIIRKCRLEELGLAGRCYLLTP 528
 447 RAETKLSVPSFKVCAYDAQMLLHCNMLNDGHNEDPSRLOHIIKMHDDYGLKQMKQLSP 506
 529 RATEAEELTCHSAEYVGHILRATEKKKTRELHRESSNFDIYICPSFACQALATGACR 588
 507 RAATIDEVCLATRAHVNTRVRLGLREPKELHDAAGITNSVYLHPRTFDCATLAAGLVQ 566
 589 LVEAVLSEGLNGAAYVRRPGRHNAEDAACGFCFNSVAVARHAAOTISGHAL-RILIVD 647
 567 AVDSVLRGSRSGICNVRRPGRHNAEDQHPHGFICFNNVLAAGYA--IRFGLELRLVQ 624
 648 WYVHNGNGQNHFEEDDPVLYVSLHRYDCTFFPMGDEGASSOIGRAAGTGFVNNAWNG 707
 625 WYVHNGNGQNHFEEDDPVLYVSLHRYDCTFFPMGDEGASSOIGRAAGTGFVNNAWNG 684
 708 PRMGADVYLAAMHRLVPLTAYEFNPETLYVSAGFDDAARGPGLGCOVSPAHNLHLM 767
 685 KMGDLIEVLAFOOLIMPLATYEFNPOLVVSAGFDALGDPGLGCVTAEGVMTLHMLS 744
 768 GLASGRITLLLEGVYVLTISSEMACTRSLLGDRPP-----LLTLPRP-----LSGALS 819
 745 ALASGRITVCLLEGVYVLTISSEMACTRSLLGDRPP-----LLTLPRP-----LSGALS 804
 820 ITETIQVHRRYKSL 834
 805 LOOCLQOVORHNRSL 819

RESULT 6

AAU00244
 ID AAU00244 standard; Protein; 363 AA.
 XX
 AC AAU00244;
 XX
 DT 18-MAY-2001 (first entry)
 XX
 DE Human histone deacetylase 6, HDAC6.
 XX
 KW Histone deacetylase-like protein; HDLP; inhibitor; crystal; cancer;
 KM three dimensional structure; protein coordinate data; HDAC6;
 KW rational drug design; histone deacetylase.
 OS Homo sapiens.
 XX
 PN WO200118045-A1.
 XX
 PD 15-MAR-2001.
 XX
 PE 08-SEP-2000; 2000WO-US24700.
 XX
 PR 08-SEP-1999; 99US-0152753.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (OTCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Pavletich N, Finnin M, Donigian J, Richon V, Rifkind RA, Marks PA;
 PI Breslow R;
 DR WPL; 2001-226741/23.
 XX
 PT A new 4 Angstrom crystal structure of an enzyme comprising deacetylase
 PT activity, where the enzyme possesses a conserved alpha/beta structure
 PT used for screening and identifying potential deacetylase inhibitor
 PT compounds -
 XX
 PS Disclosure; Fig 2; 329pp; English.
 XX
 CC The sequence represents the amino acid sequence of histone deacetylase 6
 CC (HDAC6) used to identify the sequence of histone deacetylase-like protein
 CC (HDLP) used in the course of the invention. The HDLP sequence was used to
 CC identify a potential deacetylase inhibitor compound comprising: (a) using
 CC a three dimensional (3D) structure of HDLP as defined by the atomic
 CC coordinates fully defined in the specification; (b) employing the 3D
 CC structure to design or select the potential inhibitor. A crystal of the
 CC enzyme, and its mutants, such as a Cys75Ser/Cys77Ser double mutant of
 CC HDLP, and a Tyr297Phe active site mutant of HDLP, comprising deacetylase
 CC activity was determined where the crystal diffracts x-rays for the
 CC determination of the atomic coordinates of the enzyme to a resolution
 CC greater than 4 Angstrom. The crystal is used for screening for a novel
 CC drug comprising: (a) selecting an inhibitor by performing rational drug
 CC design with the 3D structure determined from the crystal; (b) contacting
 CC the inhibitor with the ligand binding domain of the crystal; and (c)
 CC detecting the binding potential of the inhibitor for the ligand binding
 CC domain, where the novel drug is selected based on its having a greater
 CC affinity for the ligand binding domain than for the known drug. The drug
 CC may be useful for inhibition of cell growth in the treatment of cancer.
 XX
 SQ Sequence 363 AA;

Query Match 27.3%; Score 1749.5; DB 22; Length 363;
 Best Local Similarity 89.4%; Pred. No. 4.5e-131;
 Matches 363; Conservative 0; Mismatches 0; Indels 43; Gaps 14;

83 LAGTGLVLDQLENEFCLMDSPFEPGERLHAKEQLIOGLIDRCVSEFOARFEKEELM 142
 1 LAGTGLVLDQLENEF-----FPEGERLHAKEQLIOGLIDRCVSEFOARFEKEELM 52
 143 LVHSLFYDLMETTYOYNEGELRVADTYDSYLLHPNSTSCACLAGSVLRVDAVLGAE 202
 53 LVHSLFYDLMETTYOYNEGE-RVADTYDSYLLHPNSTSCACLAGSVLRVDAVLGAE 111
 203 IRNGMAIIRPGHNAHSHLMDGYCMENHVAAYAAQOKHRIIRVLLIYDMVDVHHGQGTFF 262

DB 112 -----AIIIPPHHSHSLMDGICMHNVAARVADQKH-IRRLVIVDMVDHVGOGTOP 165
OY 263 FPDOPSVLYFSIHREYQGRFMPHLKASNMSTGFGOGGYTINVMNOVGMADADYIA 322
DB 166 FPDOPSVLYFSIHREYQGRF-PHLKAS-WSTTGFGOGGYTINVMNO-GMADADYIA 222
OY 323 FHLVLLPVALLERQPOLVLAAGFDALQDPKGMMAATPAGFAQLTHLMGLAGKILSL 382
DB 223 FHLVLLPVALLERQPOLVLAAGFDALQDPKGMMAATPAGFAQLTHLMGLAGKILSL 282
OY 363 EGGYMLRALAEVGSALHTLLDPCPMLESPPGAPCSAASVSCALELEPFEVYVRS 442
DB 283 -GGYMLRALAEVGSALHTLLDPCPMLES-GAPCSAASVS-----EPFEVYVRS 334
OY 443 ETVERDNMEEDVNESEEGPWEPPVLPILTFWVLOSRTGLVYDQN 488
DB 335 ET-----EDNV-----EPVLPILTFW-LQSRGLVYDQN 363
RESULT 7
AAB42743
ID AAB42743 standard; Protein; 675 AA.
AC AAB42743;
XX
XX 08-FEB-2001 (first entry)
DE Human ORFX ORF2507 polypeptide sequence SEQ ID NO:5014.
XX
XX Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;
vulnerary; antiparietal; antiparinsonian; noctropic; neuroprotective;
anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
hypotensive; dermatological; immunosuppressive; antinflammatory;
antifungal; antineuritic; antihypertensive; antihypertensive;
antidiabetic; gene therapy; cancer; proliferative disorder; hypertension;
neurodegenerative disorder; osteoarthritis; graft vs host disease;
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
thrombosis; cartilage damage; antinflammatory disease; coagulation;
thrombosis; contraceptive.
XX
XX Homo sapiens.
OS WO200058473-A2.
XX
XX 05-OCT-2000.
XX
XX 31-MAR-2000; 2000WO-US08621.
XX
XX 31-MAR-1999; 99US-0127607.
XX 02-APR-1999; 99US-0127636.
XX 05-APR-1999; 99US-0127728.
XX 30-MAR-2000; 2000US-0540763.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinketsu RA, Leach M;
PI WPI; 2000-602362/57.
DR N-PSDB; AAC76952.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
XX useful for treating e.g. cancers, proliferative disorders,
XX neurodegenerative disorders and cardiovascular disease -
XX
XX Claim 11; Page 4195-4196; 5507pp; English.
XX
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX

CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antiparietal; antiparinsonian; noctropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antinflammatory; antibacterial; antiviral; antifungal; antineuritic;
CC antihypertensive; antidiabetic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX
XX Sequence 675 AA;
XX
XX Query Match 17.7%; Score 1132; DB 21; Length 675;
XX Best Local Similarity 36.6%; Pred. No. 2.7e-81;
XX Matches 290; Conservative 92; Mismatches 240; Indels 170; Gaps 22;
OY 69 VGLQGMDELNEARALAGTGLVDEQNEFICLMDSP-----EGPERLHAKEDLIQGL 124
DB 4 LGTGG-----DHGAMGTALVYHEDMTATLLMD--PECEIERPERLTAALDRKGL 56
OY 125 LRCVSGFOARFAKEELIMVHSLYIDIMETTYOYMGELRLVADYVLSHNSCA 184
DB 57 EQGCLILASREASEEELGLVHSPEYSLVRETVLQGELOALSGCDALYFHSSTHCA 116
OY 185 CLASGVLRVDAVLCAGETRNMAITRPGHNOHSLMDGYCMFNHVAARVADQKHRI 244
DB 117 RLAAAGLGLVDAVLCAGETRNMAITRPGHNOHSLMDGYCMFNHVAARVADQKHRI 176
OY 245 RRLVYDMVYHNGOQGFPEDOPSVLYFSIHREYQGRFMPHLKASNMSTGFGOGGYT 304
DB 177 HRLVYDMVYHNGOQGFPEDOPSVLYFSIHREYQGRFMPHLKASNMSTGFGOGGYT 236
OY 305 INVPMNOVGMADADYIAAEFLHLLPVALLERQPOLVLAAGFDALQDPKGMMAATPAGFA 364
DB 237 VNLPMNOVGMADADYIAAEFLHLLPVALLERQPOLVLAAGFDALQDPKGMMAATPAGFA 296
OY 365 QLTHLMGLAGKILSLBGGVLRALAEVGSALHTLLDPCPMLESPPGAPCR-----SA 420
DB 297 HLTQLQVLAAGVCAVLEGGYHLESVCMTVOFTLLDPAPLSGPMAPORCGSA 356
OY 421 QASVSCALELEPFEVYVRSFETVERDNMEEDVNESEEGPWEPPVLPILTFWVLOSRT 480
DB 357 LESIGSARAQAOPHMSLQOQDYTA---VPMSPSSHSPPGR--PELLD--GGPVKAA 408
OY 481 TGLVYDQNMNHNCLNDSHHPYORILRLMCRLEELGLAGRLTLPRTATB-AELLTC 539
DB 409 A-----SAPSSLDQPC-----LCRAPSVRTAVALT 435
OY 540 HSAETV-----GHLPAETKMKTR---ELHRSNMFDSITYICPTFACQALTAGAA 586
DB 436 PDITVLPDPVLIQOEASALRETEAWARPHESLAREE-----ALTLGKL 480
OY 587 CRVLEAVLSGEVLNGAAYVRPGHNAEDQACGFCFNSVYAVARAQOTISGALRLIY 646
DB 481 LYLLOGMIDGVNSGIAATPASAAATTD-----AVVRG--LSHQAORILCY 526
OY 647 DMDVHNGMGTOMFEDDPVLYVLSHRVDHGTFFPMGDSGASQIGRAAGTGTVNVMN 706
DB 527 -----ALGQLRPPDLAHGDSLWL 546
OY 707 GPRMGADADYLAAMH-----RLVLPVIAEFNDELVLVNSAGFADARGDPL 749
DB 547 NRGKRAAALSMFHVSTPLPVMTGFLSCITGLVPLAVGFGOPDVLVNLG-----PG 599

Qy	750	GGCCYSPGGYAHMLTLLMLASGRILLIE----	GGYNLTLSISEMAACTRSLGLGPPPL	803
Db	600	HGLQ-GPHN-ALLAAALRSLAGRGVALLLEEV	SWAGRCGGVGGRGGEPVAFAPPEL	657
Qy	806	LT-LPRPLSGA	816	
Db	658	HTPASRDPGPGA	669	
RESULT 8				
AAAB42757				
ID	AAAB42757	standard; Protein; 686 AA.		
XX	AAAB42757;			
AC				
XX				
DT	08-FEB-2001	(first entry)		
XX				
DE	Human ORFX ORF2521 polypeptide sequence SEQ ID NO:5042.			
XX				
KW	Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;			
KW	vulnerary; antipsoiatric; antiparkinsonian; nootropic; neuroprotective;			
KW	anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;			
KW	immunostimulant; thrombolytic; coagulant; vasootropic; antidiabetic;			
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;			
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;			
KW	antianemic; gene therapy; cancer; proliferative disorder; hypertension;			
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;			
KW	cardiovascular disease; diabetes mellitus; hypochromidism; SCID; AIDS;			
KW	cholesterol ester storage; systemic lupus erythematosus; infection;			
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;			
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;			
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;			
KW	thrombosis; contraceptive.			
KM				
XX				
OS	Homo sapiens.			
XX				
PN	WO200058473-AZ.			
XX				
PD	05-OCT-2000.			
XX				
PF	31-MAR-2000; 2000WO-US08621.			
XX				
PR	31-MAR-1999; 99US-0127607.			
PR	02-APR-1999; 99US-0127636.			
PR	05-APR-1999; 99US-0127728.			
PR	30-MAR-2000; 2000US-0540763.			
XX				
PA	(CURA-) CURAGEN CORP.			
XX				
PI	Shlunkets RA, Leach M;			
XX				
DR	WPI: 2000-602362/57.			
PR	N-PSDB; AAC76966.			
XX				
PT	Novel nucleic acids and peptides derived from open reading frame X,			
PT	useful for treating e.g. cancers, proliferative disorders,			
PT	neurodegenerative disorders and cardiovascular disease -			
XX				
PS	Clalm 11; Page 4225-4227; 5507pp; English.			
XX				
CC	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,			
CC	which represent the human ORFX open reading frames 1 to 3161. The ORFX			
CC	sequences have activities such as: cytostatic; hepatotropic; vulnerary;			
CC	antipsoiatric; antiparkinsonian; nootropic; neuroprotective;			
CC	osteoprotic; anticonvulsant; antiarthritic; immunosuppressant;			
CC	immunostimulant; cardiant; thrombolytic; coagulant; vasootropic;			
CC	antidiabetic; hypotensive; dermatological; immunosuppressive;			
CC	antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;			
CC	antithyroid; and antianemic. The sequences can be used for determining			
CC	the presence of or predisposition to, or preventing or treating			
CC	pathological conditions associated with an ORFX-associated disorder. The			
CC	nucleic acids can be used to express ORFX proteins in gene therapy			

DR N-PSDB; ABO73028.
XX Novel histone deacetylase 9 polypeptide and polynucleotide encoding the
PT polypeptides, useful for diagnosing conditions related to abnormal
PT polypeptide activity e.g., cancer, atherosclerosis, psoriasis -
XX
PS
XX Claim 1, Fig 2B; 103pp; English.
CC The present invention describes histone deacetylase (HDAC) 9 proteins
CC (1). (1) has cytostatic, antiproliferative, antiatherosclerotic and
CC antiinflammatory activities, and can be used in gene therapy and as a
CC normal transcriptional regulator. (1) can be used in the diagnosis of a
CC condition associated with abnormal HDAC9 expression or activity in a
CC human. Polynucleotides encoding (1) can be used for the diagnosis of a
CC condition associated with abnormal regulation of gene expression which
CC includes, abnormal cell proliferation, cancer, atherosclerosis,
CC inflammation, host inflammatory or immune response, or
CC psoriasis in humans which comprises detecting abnormal transcription of
CC messenger RNA transcribed from the natural endogenous human gene encoding
CC (1) in appropriate tissue or cell from a human, where the abnormal
CC transcription is diagnostic of the condition. The present sequence
CC represents human HDAC9 from the present invention.
XX
XX Sequence 673 AA:

Query Match 17.6%; Score 1125; DB 23; Length 673;
Best Local Similarity 37.2%; Pred. No. 9, 8e-81;
Matches 283; Conservative 89; Mismatches 225; Indels 164; Gaps 20;

QY 85 GTGLVLDOLNEFHCLMDSPF---EGPERLAIKEOLIOGLDRCVSFOARFAEKEE 140
DB 2 GTALVYHEMDMTRLLMD--PECEIERPERLTAALDRKRGLEKRLSARESEEE 59
QY 141 LMLVHSLEYIDMETTYQYNEGELRYLADYDSVYLHPNSYSCACIASGSLRLYDAVLG 200
DB 60 LGIVHSPEYSLVRETYQYNGKELOALSGQFDALYHFSTFCARLAAGAGLDYDAVL 119
QY 201 AEIRNGMALIRPGHHAQHSIMDGYCMFNHVAARAAQOKRIRRYLVDMVNHGOGT 260
DB 120 GAVONGIALVRRPGHGHGQRAAANGFCVFNNVAIAAHAQKHRLHRLTYDMVNHGOGI 179
QY 261 QFTFDODPSVLYFSIHREYQGRFPHILKASNMSTGFGGOGYTTINVMNQGMRADYI 320
DB 180 QYLFEDDPSVLYFSIHREYQGRFPHILKASNMSTGFGGOGYTTINVMNQGMRADYI 239
QY 321 AAFHLVLLPALIEPOPVLVVAAGFDALQDPRKGEAATPAFAOTLHLLMGLAGKLT 380
DB 240 AAFHLVLLPALIEPOPVLVVAAGFDALQDPRKGEAATPAFAOTLHLLMGLAGKLT 299
QY 381 SLEGGYNRLALAEVYSASLHTLLGDPCEPMLSPGAPCR---SAQASVSCALALEPFE 436
DB 300 VLEGGYHLESLEAESYCMVTQTLGDPAPPLSGPMAPCCQCESSALESTIOSARAAQAPHWK 359
QY 437 VLVSTETVERDNMEEDVNESEEGPWPVPLITLWVPLQSRGLYVDQMMNHNCML 496
DB 360 SLQGDQDVTAA---VPMSPSSHSPBEGRP--PPLLP--GGPVCKAAA----- 396
QY 497 DSHHEPQRIIRIKRLEELGLAGRCITLTPRPATE--AELLTCHSAEYV----- 545
DB 397 ---SAPSSILDQPC-----ICPAPSVRTVALTTPDITLVLPPDVIOQA 438
QY 546 GHILATEMKTR---ELHRESSNFDSIYICPSTFACQALATGACRLVAVVLSGEVLNA 602
DB 439 SALRETAAMAAPHESLARER---ALTALGLKLYLLDGMIDGOVNSGI 483
QY 603 AVVRRPGHHAQDACAAGFCFNSVAARNAQOTISGHALRLITVDMVNHGOGTOMFED 662
DB 484 AATPSAATAATLD-----VAVRAG--LSHGAKRLCY----- 513
QY 663 DPSVLYVSLHRYDHGTFPPMGDEGASQSIGRAAGTGFTVNVANMGPFRMGDADYLAAMH-- 720
DB 514 ---ALGQIDRPPDLAHDGRSLMLNIRGEKAAALSMFHV 549

QY 721 -----RLVLPAYEFNPETLYSAGFPAARGDPLGGGVPEGYAHLTHL 765
DB 550 TPLPMTGGFLSCITLGLVLPAYGFOPDLVALG-----PEHGLQ-GRHA-ALLAAM 600
QY 766 IMGLASGRILLIEGGYNLISSESMACYSRLSGDPPPL 806
DB 601 LRGLAGRYALALE-----NSTPQAGILARVINGEARPPL 637

RESULT 11
AAE22854
ID AAE22854 standard; Protein; 673 AA.
XX
XX AAE22854;
AC
XX
XX 21-AUG-2002 (first entry)
DT
XX
XX Human histone deacetylase protein.
DE
XX
XX Human; histone deacetylase; therapy; cancer; bait protein; cytostatic;
KW
XX
XX enzyme.
KW
XX
XX Homo sapiens.
OS
XX
XX MO200230970-A2.
PN
XX
XX 18-APR-2002.
PD
XX
XX 11-OCT-2001; 2001MO-EP11759.
PF
XX
XX 13-OCT-2000; 2000US-239928P.
PR

PA (FARB) BAYER AG.
XX
XX Zhu Z;
XX
XX WPI: 2002-416859/44.
DR
XX
XX N-PSDB; AAD36979.

PT New human histone deacetylase polypeptide useful for identifying
PT modulating agents that can be used for treating diseases such as cancer
PT
XX
XX

PS Claim 25; Fig 2; 116pp; English.

XX
XX The present invention relates to novel histone deacetylase proteins and
XX polynucleotides encoding them. Sequences of the invention are useful for
XX identifying modulating agents that are used for preventing, ameliorating,
XX treating or correcting dysfunctions or diseases such as cancer. They can
XX also be used to screen for human histone deacetylase activators and
XX inhibitors. They are useful for generating antibodies and can be used as
XX bait proteins in two-hybrid assay or three-hybrid assay. The present
XX sequence is human histone deacetylase protein.
XX
XX

SO Sequence 673 AA;

Query Match 17.6%; Score 1125; DB 23; Length 673;
Best Local Similarity 37.2%; Pred. No. 9, 8e-81;
Matches 283; Conservative 89; Mismatches 225; Indels 164; Gaps 20;

QY 85 GTGLVLDOLNEFHCLMDSPF---EGPERLAIKEOLIOGLDRCVSFOARFAEKEE 140
DB 2 GTALVYHEMDMTRLLMD--PECEIERPERLTAALDRKRGLEKRLSARESEEE 59
QY 141 LMLVHSLEYIDMETTYQYNEGELRYLADYDSVYLHPNSYSCACIASGSLRLYDAVLG 200
DB 60 LGIVHSPEYSLVRETYQYNGKELOALSGQFDALYHFSTFCARLAAGAGLDYDAVL 119
QY 201 AEIRNGMALIRPGHHAQHSIMDGYCMFNHVAARAAQOKRIRRYLVDMVNHGOGT 260
DB 120 GAVONGIALVRRPGHGHGQRAAANGFCVFNNVAIAAHAQKHRLHRLTYDMVNHGOGI 179
QY 261 QFTFDODPSVLYFSIHREYQGRFPHILKASNMSTGFGGOGYTTINVMNQGMRADYI 320

```

Db      180 QYLFEDDPSTLYTSMHRYEHRGFWPFLRESADAVGRGQGLGFTVNLFWNVGMGNADYV 239
      321 AAEHLVLLPVALFEPQPLVLAAGFDALQDQPKGEMATPAGFQQLTHLMLGAGSKLIL 380
      240 AAEHLHLLPLAFEDPFLVLSAGFDSALGDPBEGOMATPFCFHLNQLLOLVLAGGRCA 299
QY      381 SLGGYINLRALAEVGSASLHTLLGDDPCPMLESPAPCR---SAQASVSCALELEPWE 436
      300 VLEGSGHLESLAESVCMVTQTLGDPAPPLSGPMAFCORCEGSALESIOSARAQAAPHWK 359
Db      437 VLVRSTETVERDNNEEDNVESEEGPWEPPVPLILTPVYLOSTGLVYDQMMHNCNLM 496
      360 SLQOQDYTA---VPMSPSSHPEGRP--PPLLP--GGPVCKAAA----- 396
QY      497 DSHHPEVPQRLIRIMCRLEELGLAGRCILTLTPRPATE--AEILTCHSAEYV----- 545
      397 -----SAPSSLDDQPC-----LCAPASVTRVAVALTPPDITLVLPDYIQGEA 438
QY      546 GHLRATEKMKTR---ELHRESSNFDSTIYICPTFACQALATGAACRLVEAYLSGEVINGA 602
      439 SALREETEAVARPHESLAREE-----ALTFALGKLLYLIDGKLDGQVNSGI 483
QY      603 AVVRPGRHHAEDQACGCFEFSNVAAARHAQTISGHALRLIYDMDVHHNGTQHMFED 662
      484 AATPASAAATLID-----VAVRKG--LISHGAORLLCY----- 513
Db      663 DPSVLVSLHRDHTGTFEPMGDEGASSQIGRAAGTGTVAVMNGPRMGADYLAAMH-- 720
      514 -----ALGQLDPRPDLADGSGIMLNITNGKEAALSMFHV 549
QY      721 -----RLVPIAEVFNELVLSAGFDPARGDPLGGCOVSPGEGYAHYHL 765
      550 TPLPVATGGLSCILGIVLPLAYGFQPDVLYVALG-----PGHGLQ--GRHA--ALLAAM 600
QY      766 LMGLAGRIILILEGGVNLTSISESMACRSLGIDPPILL 806
      601 LKGLAGRVALLTEE---NSTPOLAGILARVINGEAPSL 637
Db

```

RESULT 12
ABBB1615
ID ABBB1615 standard; Protein; 625 AA.
AC ABBB1615;
DT 23-SEP-2002 (first entry)
XX Human HDAC9 variant HDAC9v3 protein sequence SEQ ID NO:6.
DE
XX Human; HDAC9; histone deacetylase related gene; histone deacetylase;
KW cytosolic; antiproliferative; antithrombotic; antitumor; antitumor;
KW gene therapy; transcription regulator; abnormal cell proliferation;
KW cancer; atherosclerosis; inflammatory bowel disease; inflammation;
KW immune response; enzyme.
XX Homo sapiens.
OS
PN WO200250285-A2.
XX
PD 27-JUN-2002.
XX
PE 18-DEC-2001; 2001WO-EP14928.
XX
PR 20-DEC-2000; 2000US-356827P.
PR 23-MAY-2001; 2001US-293089P.
PR 06-SEP-2001; 2001US-317984P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Cohen D, Bhatia U, Cai RL, Fischer DD;
XX

```

DR      WPI: 2002-508805/54.
DR      N-PSDB: AB073031.
XX
PT      Novel histone deacetylase 9 polypeptide and polynucleotide encoding the
PT      polypeptides, useful for diagnosing conditions related to abnormal
PT      polypeptide activity e.g., cancer, atherosclerosis, psoriasis -
XX
PS      Claim 1; Fig 14; 103pp; English.
XX
CC      The present invention describes histone deacetylase (HDAC) 9 proteins
CC      (1) (1) has cytosolic, antiproliferative, antithrombotic and
CC      antitumor activities, and can be used in gene therapy and as a
CC      normal transcription regulator. (1) can be used in the diagnosis of
CC      a condition associated with abnormal HDAC9 expression or activity in a
CC      human. Polynucleotides encoding (1) can be used for the diagnosis of a
CC      condition associated with abnormal regulation of gene expression which
CC      includes, abnormal cell proliferation, cancer, atherosclerosis,
CC      inflammatory bowel disease, host inflammatory or immune response, or
CC      psoriasis in humans which comprises detecting abnormal transcription of
CC      messenger RNA transcribed from the natural endogenous human gene encoding
CC      (1) an appropriate tissue or cell from a human, where the abnormal
CC      transcription is diagnostic of the condition. The present sequence
CC      represents the human HDAC9 variant HDAC9v3, from the present invention.
XX
SQ      Sequence 625 AA:
      15.2%; Score 970; DB 23; Length 625;
      Best Local Similarity 35.9%; Pred. No. 2,1e-68;
      Matches 250; Conservative 81; Mismatches 208; Indels 158; Gaps 22;
QY      85 GTGLVLDQLENEFHCMLDSEFP---EGPERLHAKEQLOIGLDRCVSPQARFEKEE 140
      2 GTALVYHEDMDATRLAMD--PECIEERPERFALDRNGGLBGRCLRLSARESEEE 59
Db      141 LMLVHLEYIDLMETQYMNBEGLRYLADTDSVTLHPNSYCAQLASSGYLRNDAYIG 200
      60 LGLVHSPYVSLVRETQVIGKEELQALSGQFAIYFHSFTFCARLAAGAGIOLYDAVLT 119
QY      201 AEIRNGMAIIRPGHHAOSLMDGCMFNHVAARVAQAOKRIRIRVLYDMDVHHNGOET 260
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KM autoimmune disorder; neurological disorder; metabolic disorder;
KM inflammatory disorder; cardiovascular disorder; reproductive disorder;
KM blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KM neptrotropic; anticoagulant.
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OS Homo sapiens.
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PN WO200155301-A2.
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XX 31-JAN-2000; 2000US-0179065.
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PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.

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Run on: June 6, 2003, 14:46:08 ; Search time 29 Seconds

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Title: US-09-800-187-6

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	390	6.1	335	US-09-446-504-80	Sequence 80, Appl
2	390	6.1	335	US-09-712-266-80	Sequence 80, Appl
3	292	4.6	517	US-09-282-305-8	Sequence 8, Appl1
4	290.5	4.5	439	US-09-282-305-6	Sequence 6, Appl1
5	278	4.3	458	US-09-282-305-2	Sequence 2, Appl1
6	277.5	4.3	482	US-08-528-255A-1	Sequence 1, Appl1
7	277.5	4.3	482	US-08-717-365-1	Sequence 1, Appl1
8	242	3.8	432	US-09-282-305-10	Sequence 10, Appl
9	225	3.5	351	US-09-282-305-4	Sequence 4, Appl1
10	155.5	2.4	907	US-08-783-774-2	Sequence 2, Appl1
11	155.5	2.4	907	US-09-328-599A-1	Sequence 1, Appl1
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13	150.5	2.4	878	US-09-556-706B-2	Sequence 2, Appl1
14	149.5	2.3	2137	US-09-134-001C-4463	Sequence 4, Appl1
15	145.5	2.3	2475	US-09-413-814-48	Sequence 48, Appl
16	145	2.3	4551	US-09-320-878-1	Sequence 1, Appl1
17	142	2.2	4613	US-09-105-537-31	Sequence 31, Appl
18	142	2.2	11877	US-09-105-537-6	Sequence 6, Appl1
19	137.5	2.1	1841	US-08-804-227C-6	Sequence 6, Appl1
20	137.5	2.1	5215	US-09-105-537-2	Sequence 2, Appl1
21	136.5	2.1	412	US-08-477-254A-4	Sequence 4, Appl1
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23	136.5	2.1	412	US-08-428-734B-4	Sequence 4, Appl1
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39	129.5	2.0	3739	US-09-105-537-33	Sequence 33, Appl
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41	126.5	2.0	3011	US-08-710-637-2	Sequence 2, Appl1
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44	126	2.0	344	US-08-475-634D-19	Sequence 19, Appl
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ALIGNMENTS

RESULT 1
US-09-446-504-80
Sequence 80, Application US/09446504
Patent No. 6218150
GENERAL INFORMATION:
APPLICANT: UEMORI, Takashi
APPLICANT: SATO, Yoshimi
APPLICANT: FUJITA, Tomoko
APPLICANT: MIYAKE, Kazuo
APPLICANT: MIKAI, Hiroyuki
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408PCT
CURRENT APPLICATION NUMBER: US/09/446,504
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 335
TYPE: PRT
ORGANISM: Pyrococcus furiosus
US-09-446-504-80

Query Match 6.1%; Score 390; DB 4; Length 335;
Best Local Similarity 33.7%; Pred. No. 1.1e-25;
Matches 101; Conservative 53; Mismatches 104; Indels 42; Gaps 15;

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RESULT 2
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; Patent No. 6333158
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: MIKAI, Hiroyuki
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-408BCT
; CURRENT APPLICATION NUMBER: US/09/712,266
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/446,504
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
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; TYPE: PR1
; ORGANISM: Pyrococcus furiosus
; US-09-712-266-80

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RESULT 3
US-09-282-305-8
Sequence 8, Application US/09282305
Patent No. 6287843
GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maltese Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305

:
 : CURRENT FILING DATE: 1999-03-31
 :
 : PRIOR APPLICATION NUMBER: 60/080,563
 :
 : PRIOR FILING DATE: 1998-04-03
 :
 : NUMBER OF SEQ ID NOS: 18
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 : SOFTWARE: PatentIn Ver. 2.0
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 : SEC ID NO 8
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 : LENGTH: 517
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 : TYPE: PRF
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 : ORGANISM: Zea mays
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 : US-09-282-305-8

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RESULT 4
US-09-282-305-6
; Sequence 6, Application US/09282305
; Patent NO. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Matzke Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/282,305
; CURRENT FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/080,563
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
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DB 309 LIGGGYTTIRNVARCWCYETGVALGHE--LTDKMP 342

RESULT 5
US-09-282-305-2
Sequence 2, Application US/09282305
Patent No. 6287843
GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 458
TYPE: PRF
ORGANISM: Zea mays
US-09-282-305-2

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RESULT 6
US-08-528-255A-1
Sequence 1, Application US/08528255A
Patent No. 5659016
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: FUKUKAWA, YOICHI
TITLE OF INVENTION: RPD PROTEIN AND DNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THELL, BOUTELL & TANIS, P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/528,255A
FILING DATE: September 14, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32549
REFERENCE/DOCKET NUMBER: Furuya Case 1335
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 482
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal lung cDNA library
US-08-528-255A-1

Query Match 4.3%; Score 277.5; DB 1; Length 482;
Best Local Similarity 23.8%; Pred. NO. 1.5e-15;
Matches 110; Conservative 76; Mismatches 210; Indels 67; Gaps 17;
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DB 15 YDGGVGNV--YGGGHHMKPRIRIMTNLNLNTGYRKMELYRPHKAAEEMTKYHSDY 72
OY 545 VGHIRATEKAKTRELHRESSNFDIYICP--STFACQATGAACRLVEAVLSEVING 601
DB 73 IKFLRSIRPNMSEYSKQOMRFNVEGDCPFEDGLFEFCQSLTSGS--VASAVKLKOOTD 130
OY 602 AAYVRPPG-HHAEDACGCFEFSNVAVAARHNOTISGHALRLIYDMVHNGCQHF 660
DB 131 IAVNMGGLHNAKKEASGFCYNDIVLAI--LELLKHQ-RVLYIDIDHNGDVEAF 187
OY 661 EDDPSVLYSLRYDHGTFEPMDEGASSOIGRAAGTGTVNAVNGPRMGADYLAAMH 720

DB 188 YTTDRMYVSFKY--GEYFP--GTGDLNDIGAGKGIYAVNPLR-DGIDDESYEAIK 242
OY 721 RLVLPIAYEPNELVYSAFGDAPDPLGGCOVSEGYA-----HLLHLLGLAS 771
DB 243 PYMSKVMEMFOPSAAVAVLQCGSDSLSGDRGCFNLTKGHAKCVEFKSFNLPMLMG--- 299
OY 772 GRILLILEGGYNLTSTIS-----ESMAACTRSLIGDPP-----PLTLPRPLSGAL 817
DB 300 -----GGGYTIRNVARCRITYETAVALDTEIPNELPYNDYEFYFGPDKLHISPSNMTN 352
OY 818 ASITETIQ-VHRRYRSLRVMKVEDREGPSSSKLVTKKAPOPAKPRLA--ERRTTREKKV 874
DB 353 QNTNEYLEKIKORLEPNLML-----PHAGVQMOAIPEDAIPESGDEDEDPPDKRI 405
OY 875 LEAGMK-----VTSASFEESTPGQTNSETAVALTODQ 909
DB 406 SICSSDKRIACEEFPSEDEEGGRKNSSNPKKARVATEDE 448

RESULT 7

US-08-717-365-1
Sequence 1, Application US/08717365
Patent No. 5763182
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: FUKUKAMA, YOICHI
TITLE OF INVENTION: RPDL PROTEIN AND DNA
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THEEL, BOUTELL & TANIS, P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,365
FILING DATE: 23-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/528 255
FILING DATE: September 14, 1995
APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32549
REFERENCE/DOCKET NUMBER: Furuya Case 1335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 482
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal lung cDNA library
US-08-717-365-1
Query Match 4.3%, Score 277.5; DB 1; Length 482;

Best Local Similarity 23.8%; Pred. No. 1,5e-15;
Matches 110; Conservative 76; Mismatches 210; Indels 67; Gaps 17;

OY 485 YQDNMNMHCLMDSHHPVQRLIRIMCRLEELGLAGRCVTLTPPATEALLTCHSAEY 544
DB 15 YQDGVQNT--YYQGGHPMKPHRIKMTNHLNLLANTGLVRKMEITYRPHKNAEMEKYHSDDY 72
OY 545 VGHRLATEKMKTRRELHRESSNPDSTIYCP---STPACQALATGACRLEAVNLSGEVYLG 601
DB 73 IKFLRSIRPDNMSEYKQMFQRFNVGDCPEFDLFFECQLSTGGS--VASAVKLKMQOTD 130
OY 602 AAVVREPQ--HHAQDAACGCFEFSNVAVAARNAQTISGHALRLTIYDMVDYHNGNQHM 660
DB 131 IAVNNAAGGHHAKKSAAGFCYNDIVLAI--LELIKYH-RVLYTIDIDHGDGVEAF 187
OY 661 EDDPSVLYVSLRHRYDHTFPPMGDEGASSOIGRAAGTFGVNANMGPRGADYDLAAMH 720
DB 188 YTTDRMYVSFKY--GEYFP--GTGDLNDIGAGKGIYAVNPLR-DGIDDESYEAIK 242
OY 721 RLVLPIAYEPNELVYSAFGDAPDPLGGCOVSEGYA-----HLLHLLGLAS 771
DB 243 PYMSKVMEMFOPSAAVAVLQCGSDSLSGDRGCFNLTKGHAKCVEFKSFNLPMLMG--- 299
OY 772 GRILLILEGGYNLTSTIS-----ESMAACTRSLIGDPP-----PLTLPRPLSGAL 817
DB 300 -----GGGYTIRNVARCRITYETAVALDTEIPNELPYNDYEFYFGPDKLHISPSNMTN 352
OY 818 ASITETIQ-VHRRYRSLRVMKVEDREGPSSSKLVTKKAPOPAKPRLA--ERRTTREKKV 874
DB 353 QNTNEYLEKIKORLEPNLML-----PHAGVQMOAIPEDAIPESGDEDEDPPDKRI 405
OY 875 LEAGMK-----VTSASFEESTPGQTNSETAVALTODQ 909
DB 406 SICSSDKRIACEEFPSEDEEGGRKNSSNPKKARVATEDE 448

RESULT 8

US-09-282-305-10
Sequence 10, Application US/09282305
Patent No. 6287843
GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 432
TYPE: PRT
ORGANISM: Zea mays
US-09-282-305-10

Query Match 3.8%; Score 242; DB 4; Length 432;

Best Local Similarity 25.9%; Pred. No. 1.5e-12;
Matches 87; Conservative 51; Mismatches 158; Indels 40; Gaps 13;

OY 469 LPILTWPIQSRIGLVYDQNMNMHCLMDSHHPVQRLIRIMCRLEELGLAGRCVTLTP 528
DB 5 LPITVITPIVGDGVNVY-----FGPNHMPKPHRICKTHHLVLSGLQKMEITYR 54
OY 529 RPAIEALLTCHSAEYVGHRLA---TEKMKTRRELHRESSNPDSTIYCP---STPACQAL 581
DB 55 HKAVPIELAQHSADYVEFLHRTIPDSQHLVASELTRYMLGSD---CPVFNLFEPQDI 110
OY 582 ATGA---ACRLVEAVLSEVYLGAAVVRPFGHAODAAACGCFNSVAVNAARHAQTISG 638
DB 111 YAGTIDAAARRINRHKICDAINMAGL---HNAKCEASGFCYINDIVLGI--LELLKY 164

QY 639 HALRILVDVHNGNCTOHMFEDDPVLYSLRHYDHGTFPMGDEGASSQIGRAATG 698
 165 HA-RVLYIDVHNGDEAFYTTDRMYVSFKYTG-DLEFP--GGIDIDIGERBEKY 220
 QY 699 FTVVAMNGRMDADYLAAMHRLVLPIDAVEFNPDELVSAGFPAAGDPLGCGOVSPG 758
 DB 221 YAINIPLK-DGIDTSTFRPFKTIKAVETYLPGALVLOCADSLARDLRCFNLSTEG 279
 QY 759 YALHTLMLAGSLRILILEGGYNLTISSESMAAC 794
 DB 280 HAECVRFVKF---NIPLVYGGGGYT--KENVARC 310

RESULT 9
 US-09-282-305-4
 Sequence 4, Application US/09282305
 Patent No. 6287843
 GENERAL INFORMATION:
 APPLICANT: Baldwin, Donald A.
 APPLICANT: Briggs, Steven P.
 APPLICANT: Crane, Virginia C.
 TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
 FILE REFERENCE: 5718-44,
 CURRENT APPLICATION NUMBER: US/09/282,305
 PRIOR FILING DATE: 1999-03-31
 PRIOR APPLICATION NUMBER: 60/080,563
 PRIOR FILING DATE: 1998-04-03
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 4
 LENGTH: 351
 TYPE: PRT
 ORGANISM: Zea mays
 US-09-282-305-4

Query Match 3.58; Score 225; DB 4; Length 351;
 Best Local Similarity 25.48; Pred. No. 3.3e-11;
 Matches 80; Conservative 57; Mismatches 134; Indels 44; Gaps 13;
 QY 610 HHAEDDAGCGFCFNSVAVARHAOTISGHALRILYIDMDVHNGTQHMFEEDPSVLYV 669
 46 HRAKKEASGFCYVNDIVLAI--LELIKFR-RVLYIDVHNGDEAFETTNKRVTV 102
 QY 670 SLARHDGTEFFPMGDEGASSQIGRAAGTGTNNVAMNGRMDADYLAAMHRLVLPAYE 729
 103 SPFKY--GGEFF--GGHITDVGAAEGKHVALNPLS-DGIDDTFFGLQCIIKKYMEV 157
 QY 730 FNPDELVSAGFPAAGDPLGCGOVSPGVAHLTHLMGLASGRILILEGGYNLTISSE 789
 158 YOPDVAVLQCGADSLAGDRLGCFNLVYGHADCLRFKRSY--NVMVMVLGGGGYTIIRNVAR 216
 QY 790 SMAACTRSLGDP-----PLTLPRPLSGALASITFTIQ-VHRRYKSL 834
 DB 217 CMCTEAVAVAGVDPNKLRYNDIYETFFGPDYTLHIQKSVENLTNKKMLNILENT 276
 QY 835 RVAKVE-----DREGSSSKLYTKKAPQAPKPRU---AERMTTREKKVLEAG 878
 DB 277 --SKIHVPSTQHPDRPSDEAPAEKEKEDMDKRP-PQRSRLMSGGARDSDTDEPDSLKS- 332
 QY 879 MGVVVSASFGESTP 893
 DB 333 EGKDYTFANFOMKDEP 347

RESULT 10
 US-08-783-774-2
 Sequence 2, Application US/08783774
 Patent No. 6054130
 GENERAL INFORMATION:
 APPLICANT: Spaete, Richard
 APPLICANT: Jackman, Minthrop
 TITLE OF INVENTION: NON-SPLICING VARIANTS OF

TITLE OF INVENTION: GP350/220
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036/2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PasteSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/783,774
 FILING DATE: 15-JAN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7682-037
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 907 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-783-774-2

Query Match 2.48; Score 155.5; DB 3; Length 907;
 Best Local Similarity 21.08; Pred. No. 0.00021;
 Matches 162; Conservative 87; Mismatches 292; Indels 229; Gaps 43;
 QY 484 VYDQNMAMHNCMLMPSHPEVFORILRIMCRLEELAGRCILVPRPATEALLCHSXE 543
 DB 130 VYFDVVG--TW--CHAEKMONPY-----LIEYTPYIKMDNCNSTN 169
 QY 544 YVGHRLATEKKKTRELRHRESSNFDIYICPTF-----ACAQATG----- 584
 DB 170 ITAVVBAQGLVTLPLSLPISADSNEFSVKTEMLGNEIDIECIMDELSQVLPDKNKN 229
 QY 585 AACRLVEA-VLSGEVLNCAAVRPPGHHAEQDACGFCFNSVAVARHAOTISGHALRI 643
 DB 230 ITCSGYESHVPSGILNISTSPVNP-----IPGTGVAV--SLRLTPRVSRLGNN-SI 280
 QY 644 LIVDMVHNGM-----TQHMFEDDPVLYSLRHYDHGTF-F 680
 DB 281 LTV---FYSGNGPKASGGDYCIOSNIYFSDIIPASQDPTNTTDTTVG---DNATYSV 333
 QY 681 PM-GDEGASSQIGRAAGTGTNNVAMNGRMDADYLAAMHRLVLPIDAVEFNPDELIVSA 739
 DB 334 PMVTSEDANS-----PNVTVAFWAMPNNTETDFKCKW-----TLTS- 370
 QY 740 GFDAKGDPLGCGOVSPGVA-----HLTHLMGLASGRILILEGGYNLTIS- 788
 DB 371 -----GTP--SGCENISGAFASNRTFDITVSGLGTAAP-KTILITRTATNATNTTHKVI 422
 QY 789 ESMAACTRSL-----LGDPT-----PLTLPR-----RPLSGALA 818
 DB 423 KAPSTTSPPLNTTGTGADPNTTGTGLPSSTVHPVPTNLTPASTGPTVSTADVTSPACTT 482
 QY 819 SITETIGVHRRTYKSLRYMKVDEREGSSSKLYTKKAPQAPKPRU-----ER 866
 DB 483 SGASPVTPSPPMONGTESKAPDM--TSSSTPVTPTPNATSPFAVTTTPNATSPFA 540
 QY 867 MTTREKKVLEAGMKVTSASFGESTP-----GQNSFRAVVALTQDQSEAAATGAT 919

Db 541 VTTPTNATSPVLGITSPTSAVTTPTPNATSPVLGKTSPTSAVT-----PPNAT-SPT 594

QY 920 LAOTISEAIGAMLGOTT-----SEAVGATPDQTSSEVVGAI---LDQTSSEAV 971

Db 595 LKTSPTSAV-----TTPPNATGPVGETSPQANATNHLGGSPTPVTSOPKMAT 647

QY 972 GGATLGQ-----TTSEAVGATLAQITISEAMEGAT--LDQTSSEAVGTELIQ-TP 1022

Db 648 SAVTGGHNTSSSTSSMSLRSPNPELSPSTSDNSTMPLLSAHPTEGENTQVTP 707

QY 1023 LASSTDH-QTPPTSVOGTTPOI-----SPSTLIGSLTLELGSOGASQASQAP-GEE 1074

Db 708 ASISTHVTSSPEPRPGTTSQASGPGNSSTKPGEVNVTK-GTPQMATSPQAPSQK 766

QY 1075 NLL-----GEA-----AGGQDADSMMLQSGSLDQAFY---AVTPLP 1111

Db 767 TAVPTVSTGKANSTTGKHTTG---HGARTSTPTDYGDDSTTPRP 812

RESULT 11

US-09-328-599A-1

Sequence 1, Application US/09328599A

Patent No. 6432679

GENERAL INFORMATION:

APPLICANT: MOND, James J. and Lees, Andrew

TITLE OF INVENTION: Enhancement of B Cell Activation by

TITLE OF INVENTION: Co-Ligation of Receptors for Antigen and Complement C3d

NUMBER OF INVENTION: Using EBV gp350/220 or EBV gp350/220 Peptide Adjvants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner, L.L.P.

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/328, 599A

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Fordis, Jean B.

REGISTRATION NUMBER: 32,984

REFERENCE/DOCKET NUMBER: 04995.6025-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)408-4000

TELEFAX: (202)408-4400

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 907 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-328-599A-1

Query Match 2.48; Score 155.5; DB 4; Length 907;

Best Local Similarity 21.08; Pred. No. 0.00021;

Matches 162; Conservative 87; Mismatches 292; Indels 229; Gaps 43;

QY 484 VYDQNMNHNCLMDSHHPVORILRLIMCRLEELGLAGRCUTLPRAATEELLTCHSAE 543

Db 130 VYFDVVG--TAM-CHAEKQNPY-----LIPETVPIYKWNQCNSTN 169

QY 544 YVGLRATERKTRRELHRESSNDSIYICSTF-----ACAQLANG----- 584

Db 170 ITAVVRAQGLDVTLPFLSPADSNSFVTEMLGNEIDIECIMEDGEISYVLPQDKFN 229

QY 585 AACRLVEA-VLSEGVINGAAYVRPBGHAEQDAACGCFPFNSVAVAAHQAOTISGALRI 643

Db 230 ITCSGESHVPSGGILTSTSPVATP-----IPGTAYV--SLRLPRPVSRELGN--SI 280

QY 644 LLYDMDVHHGNG-----TQHMFEDEPDSVLYSLIHRDHCFT-F 680

Db 281 LLYV-----FYSGNPKPKASGGYCIQISNIVSEDELPASQDMPTNTDITYVG---DNATYSV 333

QY 681 PM-GDEGASSQIGRAAGTFTVNVAMGPRMDADADYLAAMHRLVLPJAVEFNEDELVLSA 739

Db 334 PAVTSSEDAANS-----PVTYTAFAWAMPNNTETDEKCM-----LITS- 370

QY 740 GPDARQDPLGCGOVSPEYA-----HLTHLMGLASGRIILILEGYNLTS-----IS 768

Db 371 -----GTP-SCGENISGAFAASNRTFDIVSGIGTAP-KTLITRATATATTHKVIYS 422

QY 769 BMAACTNSL-----LQDP-----PPLTLTP-----RPLSGALA 818

Db 423 KAPESTTSPYLTNTGFPADPNTTGLPSTHVPNTLTAASGTGVSTADVTSPTPAGTT 482

QY 819 SITETIOVHRRYRSLRWKVEDREGSSSKLVTKKAPQAPARPLA-----ER 866

Db 483 SCASPVTPSPSPWDNGTESKAPDM--TSSSTPTPTPNATSPTPAVTTPTPNATSPTPA 540

QY 867 MTRKKVLEAGMGKVTASFGSESTP-----GQNSETAVALTQDQSEAAATGAT 919

Db 541 VTTPTNATSPVLGITSPTSAVTTPTPNATSPVLGKTSPTSAVT-----PPNAT-SPT 594

QY 920 LAOTISEAIGAMLGOTT-----SEAVGATPDQTSSEVVGAI---LDQTSSEAV 971

Db 595 LKTSPTSAV-----TTPPNATGPVGETSPQANATNHLGGSPTPVTSOPKMAT 647

QY 972 GGATLGQ-----TTSEAVGATLAQITISEAMEGAT--LDQTSSEAVGTELIQ-TP 1022

Db 648 SAVTGGHNTSSSTSSMSLRSPNPELSPSTSDNSTMPLLSAHPTEGENTQVTP 707

QY 1023 LASSTDH-QTPPTSVOGTTPOI-----SPSTLIGSLTLELGSOGASQASQAP-GEE 1074

Db 708 ASISTHVTSSPEPRPGTTSQASGPGNSSTKPGEVNVTK-GTPQMATSPQAPSQK 766

QY 1075 NLL-----GEA-----AGGQDADSMMLQSGSLDQAFY---AVTPLP 1111

Db 767 TAVPTVSTGKANSTTGKHTTG---HGARTSTPTDYGDDSTTPRP 812

RESULT 12

PCT-US95-04611A-19

Sequence 19, Application PC/TUS9504611A

GENERAL INFORMATION:

APPLICANT: Spaete, Richard and Jackman, Winthrop, T.

TITLE OF INVENTION: Non Splicing Variants of gp350/220

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04611A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/229, 291

FILING DATE: April 18, 1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Luann Cseer
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: AVIR-003/0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5163
 TELEFAX: 415-857-0663
 TELEX: 380816 CooleyPA
 INFORMATION FOR SEQ ID NO. 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 907 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-04611A-19

Query Match 2.4%; Score 155.5; DB 5; Length 907;
 Best Local Similarity 21.0%; Pred. No. 0.00021;
 Matches 162; Conservative 87; Mismatches 292; Indels 229; Gaps 43;

484 YTDONMANNHCLMDSHHEPVRILRIMCRLEELGLAGRCILTPRPATEALLTCHSAE 543
 130 VYFQDVFQ--TMM-CHHAEMQNPVY-----LIPETVPIKMDNCNSTN 169
 544 YVGHILATEKMTRELHRESSNDSIYICPSTF-----ACAQLATG----- 584
 170 ITAVVRAQGLDVTLPILPTSAODSNFVKTMLGNEIDIECIMDEGEISQVLPQDNKFN 229
 585 AACRLVEA-VLSGEVLNGAAVVRPGHHAEDDAGCFPFNSVAVAARHQAOTISGHALRI 643
 230 ITCGESHVPSGGILITSTSPVATP-----IPGTGAY--SLRLPRVPSRLGNP-SI 280
 644 LIVDMVHHNG-----TQHMEDDPSVLYSLHRYDHGTF-F 680
 281 LYV---FYSGNGPKASGSDYCIQSNIVFSEDEIPASQDMPTNTDITYG---DNATYSV 333
 681 PM-GDEGASSQIGRAAGTFYVAVNANGPMGDADYLAAMHRLVLAIFENBELVYVSA 739
 334 PAVTSEDANS-----PNVTYAFWAMPNNTETDFCKW-----TLTS- 370
 740 GFDAARGLDGLGCOVSPEGYA-----HLTHLMGLASGRILILEGGYNLTS-----IS 788
 371 -----GTF-SCGENISGAFASNRFTDIVSGIGTAP-KTLLITRTATNATTTTHKYIFS 422
 789 ESMACRSL-----LQDP-----PPLTLTP-----RPLSGALA 818
 423 KAPESTTSPPLNTGTFADPNTTGLPSTHVPNTLTAASGTGVSTADVTSPTPAGTT 482
 819 SITETIOVHRKRWISLRKMKVEDREGPSSSKLVTKKAPAKPRLA-----ER 866
 483 SGASPVTPSPSPMDNTESEKAPDM--TSTSTPVTTPPTPNATSPRAVTTPTPNATSPRA 540
 867 MTPREKVLKMGKVTASASGEESTP-----GQTSERAVVALTDQOSEATGAT 919
 541 VTTPTPNATSPPLTKTSTSAVTTPTPNATSPPLTKTSTSAVTT-----PPTNAT-SPT 594
 920 LAQTISEAIGAMIGOTT-----SEAVGATPDQTSSEETVGAI---LDQTSSEAV 971
 595 LKGTSPISAV-----TTPPNATGPTVGETSQAANAHTNLGISTPTPVYTSOPKNA 647
 972 GGATLGO-----TTSSEAVGATLAQTISEAAMEGAT--LDQTSSEAPGTELIQ-TP 1022
 648 SAVTTGQHNTTSSSTSSMLRSPSNPRTLSSTSDNSTSHMPLLSAHTGENTITQVTP 707
 1023 LASTTDH-QTPPTSPVQCTPQI-----SPTSLIGSLRTLELSESGASESQAAP-GE 1074
 708 ASISTHVTSSSPRPGTTSQASGPGNSSSTKRGENVNTRK-GTPPNATSPQAPSPGOK 766
 1075 NL-----GEA---AGQDMADSMMLQSGRGLDQAIY---AVPPLP 1111
 767 TAVPTVSTGKANKSTGKHTTG-----HGARTSTETPTDYGGSSTTPRP 812

RESULT 13

US-09-556-706B-2

Sequence 2, Application US/09556706B

Patent No. 6458364

GENERAL INFORMATION:

APPLICANT: Spaete, Richard

APPLICANT: Jackman, Winthrop

TITLE OF INVENTION: NON SPLICING VARIANTS OF GP350/220

FILE REFERENCE: 7682-050-999

CURRENT APPLICATION NUMBER: US/09/556,706B

CURRENT FILING DATE: 2000-04-24

PRIOR APPLICATION NUMBER: 08/783,774

PRIOR FILING DATE: 1997-01-15

PRIOR APPLICATION NUMBER: 08/229,291

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 878

TYPE: PR

ORGANISM: Virus

FEATURE:

OTHER INFORMATION: gp350

US-09-556-706B-2

Query Match 2.4%; Score 150.5; DB 4; Length 878;
 Best Local Similarity 21.7%; Pred. No. 0.00053;
 Matches 163; Conservative 79; Mismatches 297; Indels 213; Gaps 42;

484 YTDONMANNHCLMDSHHEPVRILRIMCRLEELGLAGRCILTPRPATEALLTCHSAE 543
 130 VYFQDVFQ--TMM-CHHAEMQNPVY-----LIPETVPIKMDNCNSTN 169
 544 YVGHILATEKMTRELHRESSNDSIYICPSTF-----ACAQLATG----- 584
 170 ITAVVRAQGLDVTLPILPTSAODSNFVKTMLGNEIDIECIMDEGEISQVLPQDNKFN 229
 585 AACRLVEA-VLSGEVLNGAAVVRPGHHAEDDAGCFPFNSVAVAARHQAOTISGHALRI 643
 230 ITCGESHVPSGGILITSTSPVATP-----IPGTGAY--SLRLPRVPSRLGNP-SI 280
 644 LIVDMVHHNG-----TQHMEDDPSVLYSLHRYDHGTF-F 680
 281 LYV---FYSGNGPKASGSDYCIQSNIVFSEDEIPASQDMPTNTDITYG---DNATYSV 333
 681 PM-GDEGASSQIGRAAGTFYVAVNANGPMGDADYLAAMHRLVLAIFENBELVYVSA 739
 334 PAVTSEDANS-----PNVTYAFWAMPNNTETDFCKW-----TLTS- 370
 740 GFDAARGLDGLGCOVSPEGYA-----HLTHLMGLASGRILILEGGYNLTS-----IS 788
 371 -----GTF-SCGENISGAFASNRFTDIVSGIGTAP-KTLLITRTATNATTTTHKYIFS 422
 789 ESMACRSL-----LQDP-----PPLTLTP-----RPLSGALA 818
 423 KAPESTTSPPLNTGTFADPNTTGLPSTHVPNTLTAASGTGVSTADVTSPTPAGTT 482
 819 SITETIOVHRKRWISLRKMKVEDREGPSSSKLVTKKAPAKPRLAEMRTREKKVLEAG 878
 483 SGASPVTPSPSPMDNTESEKAPDM--TSTSTPVTTPPTPNATSPRAVTTPTPNATSPRA 540
 879 MGVTSASASGEESTPQOTSEAVVALTDQOSEATGATLAQTISEAAI-----GG 931
 539 PAVTTPTPNATSPPLTKTSTSAVTT-----PPTNAT-SPTLAKTSPTSATVTTPTPNATS 552
 932 AMIGQTSSEAVGATPDQTSSEETVGAIILDQTSSEAVGATLIGQTSSEAV---GG 987
 593 PTLGKTSPTSATVTTPTPNAT-----GPTVGETSQAANAHTNLGISTPTPVYTSOPKNA 645
 968 ATLAQTISE---AAMEGATLDQTSSEAP---GTELIQ-TPLASTDH-QTPPTSPVQ 1039
 646 ATSAVTTGQHNPSSNPRTLSSTSDNSTSHMGENITQVTPASISTHVTSSSPRPG 705

QY 1040 TTPQI-----SPSTLIGSLRTLEIGSESGASQASQAP-GEENLL-----GEA---AG 1082
 Db 706 TTSQASGPGNSSTSTKGEVAVTK-CGTPQNAISQASGQKAVTPTSTGKANSTTG 764
 QY 1083 GQMDADSMLOGSNGLDQALFY--AVTPIP 1111
 Db 765 GKHTTG---HGARTSTPTDYGDSDTTPRP 792

RESULT 14
 US-09-134-001C-4463
 Sequence 4463, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 PRIOR FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 4463
 LENGTH: 2137
 TYPE: PRN
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4463

Query Match 2.3%, Score 149.5; DB 4; Length 2137;
 Best Local Similarity 21.3%; Pred. No. 0.003;
 Matches 68; Conservative 58; Mismatches 168; Indels 25; Gaps 6;
 QY 785 TSISESMACTRSLLGDPPLTLPRPLSGALASITETIOVHRRYSLRMKVEDREG 844
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 QY 965 TTSSEAVGATLQOTTSEAVGATLAOTISEAAMGATLDDOTTSEAPGTELIQTPLA 1024
 Db 1054 STS-----TSLSGSTASSTSDASSTSTSESDSTSTSLSESTSTSLSGSTST 1101
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 Db 1102 STSDSASTSTSESDSTSESTSTSESLSTSVSDSTSTSTSEASASTSTSESNASASTSLSG 1161
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RESULT 15
 US-09-413-814-48
 Sequence 48, Application US/09413814
 Patent No. 6225064
 GENERAL INFORMATION:
 APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 APPLICANT: Bristol-Myers Squibb, Co.
 APPLICANT: Beyer, Stefan
 APPLICANT: Bioecker, Helmut
 APPLICANT: Brandt, Petra
 APPLICANT: Cino, Paul M
 APPLICANT: Dougherty, Brian A
 APPLICANT: Goldberg, Steven L

APPLICANT: Hofle, Gerhard
 APPLICANT: Mueller, Joachim
 APPLICANT: Reichenbach, Hans
 TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
 TITLE OF INVENTION: heteropolyketide compounds
 FILE REFERENCE: PCN/US 99/23535
 CURRENT APPLICATION NUMBER: US/09/413,814
 EARLIER FILING DATE: 1999-10-07
 EARLIER APPLICATION NUMBER: DE 198 46 493.2
 EARLIER FILING DATE: 1998-10-09
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 48
 LENGTH: 2475
 TYPE: PRN
 ORGANISM: Sorangium cellulosum
 US-09-413-814-48

Query Match 2.3%, Score 145.5; DB 4; Length 2475;
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 QY 275 IHREYQGRFWP---HLKASNWTG--FGOGGYTINPVNVOGMRADYIAFLH----- 325
 Db 217 ---YREGTINSPDCHCRFADDAAGTIFGDGVILKRYKD-ALRQGDHYAVYKGSAT 272
 QY 326 -----VLLPVAL---EPQPOLV--LVAAGEDALOGDPRGEMAAATPA 361
 Db 273 NSDGRKRYVYAPKSGGVAVIRAAALAAQVEPTIRFEVHAGTGLAGDPI-EVEALTE 331
 QY 362 GFAQ-----LTLH--LMGLAG-KILSLGGYNLRALEGSASLHTLIG 404
 Db 332 VFAAGRGTCALSGVKTNIGLIDVAAGVAGIKAVLADE-----RRVLPPSLHFVRP 383
 QY 405 DPCMLSPGAPCSAASVSCALELEPFVEVLVRSSTET-----VERDMMEDNVDES 458
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 QY 459 EEEGP-----WEPPVPLITWPVLOSRTGLVYDDNMNHNLMDSHPEVPORLIRI 510
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 QY 672 HRYDHGTFPMGDEGASSQIGRAAGTFTVN-----VAMGPRMGADYLAAMHRLVPI 726
 Db 614 -----SRGLGQGVVLAESLSLEQALALVLCQTPVPGDA--TPQRERLVRTL 659
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 Db 777 PFVRYVITPTIGDPLRGAGA-----EDDLIASASASAGSPPEPSA 815

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 14:49:28 ; Search time 56 Seconds
(without alignments)
2239,945 Million cell updates/sec

Title: US-09-800-187-6

Perfect score: 6397

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 segs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6397	100.0	1215	US-09-976-280A-4	Sequence 4, Appl1
2	6397	100.0	1215	US-09-976-280A-22	Sequence 22, Appl1
3	6397	99.7	1215	US-09-817-913-11	Sequence 11, Appl1
4	6375	99.7	1215	US-09-817-538-11	Sequence 11, Appl1
5	1125	17.6	673	US-09-976-280A-2	Sequence 2, Appl1
6	809	12.6	687	US-09-976-280A-3	Sequence 3, Appl1
7	805.5	12.6	967	US-09-563-728A-30	Sequence 30, Appl1
8	805.5	12.6	1084	US-10-072-094-7	Sequence 7, Appl1
9	805.5	12.6	1084	US-10-173-539-12	Sequence 12, Appl1
10	801.5	12.5	967	US-09-817-913-7	Sequence 7, Appl1
11	801.5	12.5	967	US-09-817-538-7	Sequence 7, Appl1
12	788	12.3	706	US-10-072-094-6	Sequence 6, Appl1
13	778.5	12.2	716	US-09-563-728A-32	Sequence 32, Appl1
14	778.5	12.2	1122	US-10-072-094-8	Sequence 8, Appl1
15	778.5	12.2	1122	US-10-072-094-91	Sequence 91, Appl1
16	767.5	12.0	717	US-09-817-913-9	Sequence 9, Appl1
17	767.5	12.0	717	US-09-817-538-9	Sequence 9, Appl1
18	763	11.9	780	US-10-072-094-93	Sequence 93, Appl1
19	763	11.9	1069	US-10-072-094-87	Sequence 87, Appl1

20	755.5	11.8	855	10	US-09-817-913-13	Sequence 13, Appl1
21	755.5	11.8	855	10	US-09-817-538-13	Sequence 13, Appl1
22	750.5	11.7	855	9	US-10-072-094-9	Sequence 9, Appl1
23	722	11.3	967	9	US-10-173-539-6	Sequence 6, Appl1
24	722	11.3	1011	9	US-10-072-094-89	Sequence 89, Appl1
25	722	11.3	1011	9	US-10-173-539-2	Sequence 2, Appl1
26	619.5	9.7	1141	9	US-10-072-094-107	Sequence 107, Appl1
27	561.5	8.8	342	9	US-09-911-150-4	Sequence 4, Appl1
28	419	6.5	835	9	US-10-173-539-8	Sequence 8, Appl1
29	419	6.5	835	9	US-10-072-094-90	Sequence 90, Appl1
30	419	6.5	879	9	US-10-072-094-4	Sequence 4, Appl1
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32	390	6.1	335	10	US-09-971-309-80	Sequence 80, Appl1
33	292	4.6	517	10	US-09-883-720-8	Sequence 8, Appl1
34	291	4.5	377	10	US-09-784-877-2	Sequence 2, Appl1
35	291	4.5	377	10	US-09-817-913-15	Sequence 15, Appl1
36	290.5	4.5	377	10	US-09-817-538-15	Sequence 15, Appl1
37	290.5	4.5	344	10	US-09-883-720-6	Sequence 6, Appl1
38	286.5	4.5	344	10	US-09-815-242-5059	Sequence 5059, Appl1
39	286	4.5	150	9	US-09-911-150-6	Sequence 6, Appl1
40	278	4.3	458	10	US-09-883-720-2	Sequence 2, Appl1
41	277.5	4.3	482	9	US-09-563-728A-24	Sequence 24, Appl1
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43	277	4.3	481	10	US-09-817-913-1	Sequence 1, Appl1
44	277	4.3	481	10	US-09-817-538-1	Sequence 1, Appl1
45	277	4.3	576	10	US-09-347-331-11	Sequence 11, Appl1

ALIGNMENTS

RESULT 1	US-09-976-280A-4	Sequence 4, Application US/0976280A
1	Sequence 4, Application US/0976280A	
2	Patent No. US20020115177A1	
3	GENERAL INFORMATION:	
4	APPLICANT: Zhu, Zhimin	
5	TITLE OF INVENTION: Regulation of Human Histone Deacetylase	
6	FILE REFERENCE: 004974.00590	
7	CURRENT APPLICATION NUMBER: US/09/976, 280A	
8	CURRENT FILING DATE: 2001-10-15	
9	PRIOR APPLICATION NUMBER: US 60/239, 928	
10	PRIOR FILING DATE: 2000-10-13	
11	NUMBER OF SEQ ID NOS: 25	
12	SOFTWARE: FastSeq for Windows Version 4.0	
13	SEQ ID NO 4	
14	LENGTH: 1215	
15	TYPE: PRT	
16	ORGANISM: Homo sapiens	
17	US-09-976-280A-4	
18	Query Match	100.0%; Score 6397; DB 10; Length 1215;
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Qy      481 TGLVYDONMNNHCLNLDSSHREYFORILRLMCRLEELGLAGRCITLTPRPAATELITCH 540
Db      481 TGLVYDONMNNHCLNLDSSHREYFORILRLMCRLEELGLAGRCITLTPRPAATELITCH 540
Qy      541 SAETVGHILRATEMKTRRELHRESSNFDSTIYICPSTFACQALATGAACRLVEAVLSGEVLN 600
Db      541 SAETVGHILRATEMKTRRELHRESSNFDSTIYICPSTFACQALATGAACRLVEAVLSGEVLN 600
Qy      601 GAAYVRRPGHHAQODAACGCFPNVAVAARHAQOTISGHALRILLYDMVHNGGTOMH 660
Db      601 GAAYVRRPGHHAQODAACGCFPNVAVAARHAQOTISGHALRILLYDMVHNGGTOMH 660
Qy      661 EDDPSVLYSLHRYDGTGTFPMGDGASSQIGRAAGTGFTVNAAMNPRMGDDYLAAMH 720
Db      661 EDDPSVLYSLHRYDGTGTFPMGDGASSQIGRAAGTGFTVNAAMNPRMGDDYLAAMH 720
Qy      721 RLVLPIAYEFNPBELVLYSAGFDAARDPLJGCGVSPBGVAHLTHLMGLASGRITLLEG 780
Db      721 RLVLPIAYEFNPBELVLYSAGFDAARDPLJGCGVSPBGVAHLTHLMGLASGRITLLEG 780
Qy      781 GYNLTSISSMACSTRSLGDPPLTLTPRPPLSGALASTETITOVHRRYWSLRVAKVE 840
Db      781 GYNLTSISSMACSTRSLGDPPLTLTPRPPLSGALASTETITOVHRRYWSLRVAKVE 840
Qy      841 DREGSSSKLVTKKAPAKPRLAEEMTRERKLYLEAGMGKVSASFGSESTGOTNSET 900
Db      841 DREGSSSKLVTKKAPAKPRLAEEMTRERKLYLEAGMGKVSASFGSESTGOTNSET 900
Qy      901 AVVALTODOPSEAAATGATLAOTISEAIGAMLGOTTSEAVGATPPDOTSEETVGA 960
Db      901 AVVALTODOPSEAAATGATLAOTISEAIGAMLGOTTSEAVGATPPDOTSEETVGA 960
Qy      961 ILLDOTTSEAVGATLGOTTSEAVGATLAOTISEAAMEGATLIDOTTSEABGTGLIO 1020
Db      961 ILLDOTTSEAVGATLGOTTSEAVGATLAOTISEAAMEGATLIDOTTSEABGTGLIO 1020
Qy      1021 TPLASTDHQRPPTSPVOGTTPQISPTLIGSLRTELIGSESGASESQAPEGENLGER 1080
Db      1021 TPLASTDHQRPPTSPVOGTTPQISPTLIGSLRTELIGSESGASESQAPEGENLGER 1080
Qy      1081 AGGODMADSMMLQSGRLTDOAIFYAVRPLPWCPRHLVAVCPIPAGLIDVTPQCGDCGCTIO 1140
Db      1081 AGGODMADSMMLQSGRLTDOAIFYAVRPLPWCPRHLVAVCPIPAGLIDVTPQCGDCGCTIO 1140
Qy      1141 ENMVCLSCYQYCGRTINGHMLQHHGNSGHPVLSTIDLSAMCYCQAVVHHQALLDVN 1200
Db      1141 ENMVCLSCYQYCGRTINGHMLQHHGNSGHPVLSTIDLSAMCYCQAVVHHQALLDVN 1200
Qy      1201 IAHONKFGEDMHPH 1215
Db      1201 IAHONKFGEDMHPH 1215

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RESULT 2
US-09-976-280A-22

; Sequence 22, Application US/09976280A
; Patent No. US20020115177A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhimin

```

; TITLE OF INVENTION: Regulation of Human Histone Deacetylase
; FILE REFERENCE: 004974.00590
; CURRENT APPLICATION NUMBER: US/09/976.280A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,928
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 1215
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-976-280A-22

Query Match      100.0%; Score 6397; DB 10; Length 1215;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MTSFGDSTTRORRRONPQSPPODSSVTSKRNIKKGAVPRSTPNLAEVYKKKKKATLG 60
Db      1 MTSFGDSTTRORRRONPQSPPODSSVTSKRNIKKGAVPRSTPNLAEVYKKKKKATLG 60
Qy      61 QAMEEDLIVGLQMDLMEALAGTGLVDEQLENEFHCLMDDSPPEGPERLHAKEOLI 120
Db      61 QAMEEDLIVGLQMDLMEALAGTGLVDEQLENEFHCLMDDSPPEGPERLHAKEOLI 120
Qy      121 QEGLLDRCVSFOARFAKEELIMVHSEYIDLMETTOYMBGELRVADTYDSYLAHNS 180
Db      121 QEGLLDRCVSFOARFAKEELIMVHSEYIDLMETTOYMBGELRVADTYDSYLAHNS 180
Qy      181 YSCCLASGSVLRVYDAVLAETINGAAITRPCHHQAHSIMDGYCMFNHVAARVAAQ 240
Db      181 YSCCLASGSVLRVYDAVLAETINGAAITRPCHHQAHSIMDGYCMFNHVAARVAAQ 240
Qy      241 KHRIRVLYDMVHNGOGTQTFDODPSVLYFSIHRYEGRFPHLKAAMSTGFGG 300
Db      241 KHRIRVLYDMVHNGOGTQTFDODPSVLYFSIHRYEGRFPHLKAAMSTGFGG 300
Qy      301 OGTTINPNNQVGRADADYIAAFLHVLPALEFOPOLVVAAGFDALOGPKEMATP 360
Db      301 OGTTINPNNQVGRADADYIAAFLHVLPALEFOPOLVVAAGFDALOGPKEMATP 360
Qy      361 AGFAOLTHLMGLAGKLLISLEGYMLRALAEVSASLHTLLGDPMPLESPPACRSA 420
Db      361 AGFAOLTHLMGLAGKLLISLEGYMLRALAEVSASLHTLLGDPMPLESPPACRSA 420
Qy      421 QASVSCALELPEFWEVLVSTETVERDNNEEDNEVESEEGPEPVLPLTPVYQSR 480
Db      421 QASVSCALELPEFWEVLVSTETVERDNNEEDNEVESEEGPEPVLPLTPVYQSR 480
Qy      481 TGLVYDONMNNHCLNLDSSHREYFORILRLMCRLEELGLAGRCITLTPRPAATELITCH 540
Db      481 TGLVYDONMNNHCLNLDSSHREYFORILRLMCRLEELGLAGRCITLTPRPAATELITCH 540
Qy      541 SAETVGHILRATEMKTRRELHRESSNFDSTIYICPSTFACQALATGAACRLVEAVLSGEVLN 600
Db      541 SAETVGHILRATEMKTRRELHRESSNFDSTIYICPSTFACQALATGAACRLVEAVLSGEVLN 600
Qy      601 GAAYVRRPGHHAQODAACGCFPNVAVAARHAQOTISGHALRILLYDMVHNGGTOMH 660
Db      601 GAAYVRRPGHHAQODAACGCFPNVAVAARHAQOTISGHALRILLYDMVHNGGTOMH 660
Qy      661 EDDPSVLYSLHRYDGTGTFPMGDGASSQIGRAAGTGFTVNAAMNPRMGDDYLAAMH 720
Db      661 EDDPSVLYSLHRYDGTGTFPMGDGASSQIGRAAGTGFTVNAAMNPRMGDDYLAAMH 720
Qy      721 RLVLPIAYEFNPBELVLYSAGFDAARDPLJGCGVSPBGVAHLTHLMGLASGRITLLEG 780
Db      721 RLVLPIAYEFNPBELVLYSAGFDAARDPLJGCGVSPBGVAHLTHLMGLASGRITLLEG 780
Qy      781 GYNLTSISSMACSTRSLGDPPLTLTPRPPLSGALASTETITOVHRRYWSLRVAKVE 840
Db      781 GYNLTSISSMACSTRSLGDPPLTLTPRPPLSGALASTETITOVHRRYWSLRVAKVE 840

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QY 841 DREGSSSKLVTKKAPOPAKPRLAERMTRREKKVLEAGMKVTSASFGSESTPGQTNSET 900
| | | | |
Db 841 DREGSSSKLVTKKAPOPAKPRLAERMTRREKKVLEAGMKVTSASFGSESTPGQTNSET 900
QY 901 AVVALTODQPSSEATGATLAQTISEAAGMIGQTTSEAVGATPDQTTSEETVGA 960
| | | | |
Db 901 AVVALTODQPSSEATGATLAQTISEAAGMIGQTTSEAVGATPDQTTSEETVGA 960
QY 961 ILDOQTSEDVAVGATLGQTTSEAVGATLAQTISEAAMEGATLDQTTSEAPGTELLIO 1020
| | | | |
Db 961 ILDOQTSEDVAVGATLGQTTSEAVGATLAQTISEAAMEGATLDQTTSEAPGTELLIO 1020
QY 1021 TPLASSTHDTPTSPVQGTTPQISPTLSLRLLEGSQGSQASQAPGEENLLEGA 1080
| | | | |
Db 1021 TPLASSTHDTPTSPVQGTTPQISPTLSLRLLEGSQGSQASQAPGEENLLEGA 1080
QY 1081 AGGODMADSMLOGSRGLTDQAIFYATPLPMPCHLVAVCPIPAAGLDVTPCGDCGTIO 1140
| | | | |
Db 1081 AGGODMADSMLOGSRGLTDQAIFYATPLPMPCHLVAVCPIPAAGLDVTPCGDCGTIO 1140
QY 1141 ENNVCLSCYQYCGRYINGHMLQHHGNSGHPVLVSYDLSAMCYCQAVYHHQALLDVKN 1200
| | | | |
Db 1141 ENNVCLSCYQYCGRYINGHMLQHHGNSGHPVLVSYDLSAMCYCQAVYHHQALLDVKN 1200
QY 1201 IAHONKRGEDMPHPH 1215
| | | | |
Db 1201 IAHONKRGEDMPHPH 1215

RESULT 3
US-09-817-913-11
; Sequence 11, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besteman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817, 913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1215
; TYPE: PRT
; ORGANISM: Human
US-09-817-913-11

Query Match 99.7%; Score 6375; DB 10; Length 1215;
Best local Similarity 99.3%; Pred. No. 0;
Matches 1206; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTGDSSTTRRRSRONPOSPPODSVTSKRNIRKGAVPRSIPNLAEVKKKMKKLG 60
| | | | |
Db 1 MSTGDSSTTRRRSRONPOSPPODSVTSKRNIRKGAVPRSIPNLAEVKKKMKKLG 60
QY 61 QAMEEDLIYGLQMDLLEBALAGTGLVDEOLNEFHCLMDSFPEGPERLHAIRKQLI 120
| | | | |
Db 61 QAMEEDLIYGLQMDLLEBALAGTGLVDEOLNEFHCLMDSFPEGPERLHAIRKQLI 120
QY 121 QEBGLDRCVSFOARPEKEKELMLVHSLLEYIDIMETQYMNNEGELRYLADTYDSYLLPNS 180
| | | | |
Db 121 QEBGLDRCVSFOARPEKEKELMLVHSLLEYIDIMETQYMNNEGELRYLADTYDSYLLPNS 180
QY 181 YSCACLASGSVLRVLVAVLGAETIRNGMAIIRPGHNAQHSIMDQYCFNHNVAARYAQO 240
| | | | |
Db 181 YSCACLASGSVLRVLVAVLGAETIRNGMAIIRPGHNAQHSIMDQYCFNHNVAARYAQO 240
QY 241 KHRIRRVLLVDMVDVHHGQGTQTFDDPSVLYFSIHRYEQGRFWPHLKASNMSTGFGOG 300
| | | | |

Db 241 KHRIRRVLLVDMVDVHHGQGTQTFDDPSVLYFSIHRYEQGRFWPHLKASNMSTGFGOG 300
| | | | |
QY 301 QGYTINVPNNQGMADADYIAAFILHVLLEFOPOLVLYAAGFALOGDPGEMAAATP 360
| | | | |
Db 301 QGYTINVPNNQGMADADYIAAFILHVLLEFOPOLVLYAAGFALOGDPGEMAAATP 360
QY 361 AGFAOLTHILMLAGCKLLSLEGYNLRALAEVGSASLHTLLGDPCPMLESFAPCRSA 420
| | | | |
Db 361 AGFAOLTHILMLAGCKLLSLEGYNLRALAEVGSASLHTLLGDPCPMLESFAPCRSA 420
QY 421 QASVSCALALEPPEVLYRSTETVERDMMEDNVESEEGEPWEPVLPILTWPYQSR 480
| | | | |
Db 421 QASVSCALALEPPEVLYRSTETVERDMMEDNVESEEGEPWEPVLPILTWPYQSR 480
QY 481 TGLVYDQNMNNCINLMDSHHPVORILRIMCRLEBLGAGRCLTTPPATPAELLTCH 540
| | | | |
Db 481 TGLVYDQNMNNCINLMDSHHPVORILRIMCRLEBLGAGRCLTTPPATPAELLTCH 540
QY 541 SAEVGHILRAVEKMTRELHRESSNFDIYICPSTFACAOLATGAACRLVEAVLSEVLN 600
| | | | |
Db 541 SAEVGHILRAVEKMTRELHRESSNFDIYICPSTFACAOLATGAACRLVEAVLSEVLN 600
QY 601 GAAVVRPPGHNAEDQACGFCFFNSVYAAARAQTI SGHALRLIYDMVYHHGNGTOHMF 660
| | | | |
Db 601 GAAVVRPPGHNAEDQACGFCFFNSVYAAARAQTI SGHALRLIYDMVYHHGNGTOHMF 660
QY 661 EDDPSVLYSLHRHYDGFEPFGDGSASQIGRAAGTGTVANVAMNPRMGADYLAANH 720
| | | | |
Db 661 EDDPSVLYSLHRHYDGFEPFGDGSASQIGRAAGTGTVANVAMNPRMGADYLAANH 720
QY 721 RLVLPIAYEFNDELVLVSGFEDARGDPLGCGOVSPGEGYAHNLHILMLGASRIILLEG 780
| | | | |
Db 721 RLVLPIAYEFNDELVLVSGFEDARGDPLGCGOVSPGEGYAHNLHILMLGASRIILLEG 780
QY 781 GYNLTSISESMAACTRSLIGDPPPLTLPRLPSGALASITETIOVHRRYWSLRVAKYE 840
| | | | |
Db 781 GYNLTSISESMAACTRSLIGDPPPLTLPRLPSGALASITETIOVHRRYWSLRVAKYE 840
QY 841 DREGSSSKLVTKKAPOPAKPRLAERMTRREKKVLEAGMKVTSASFGSESTPGQTNSET 900
| | | | |
Db 841 DREGSSSKLVTKKAPOPAKPRLAERMTRREKKVLEAGMKVTSASFGSESTPGQTNSET 900
QY 901 AVVALTODQPSSEAAAGATLAQTISEAAGMIGQTTSEAVGATPDQTTSEETVGA 960
| | | | |
Db 901 AVVALTODQPSSEAAAGATLAQTISEAAGMIGQTTSEAVGATPDQTTSEETVGA 960
QY 961 ILDOQTSEDVAVGATLGQTTSEAVGATLAQTISEAAMEGATLDQTTSEAPGTELLIO 1020
| | | | |
Db 961 ILDOQTSEDVAVGATLGQTTSEAVGATLAQTISEAAMEGATLDQTTSEAPGTELLIO 1020
QY 1021 TPLASSTHDTPTSPVQGTTPQISPTLSLRLLEGSQGSQASQAPGEENLLEGA 1080
| | | | |
Db 1021 TPLASSTHDTPTSPVQGTTPQISPTLSLRLLEGSQGSQASQAPGEENLLEGA 1080
QY 1081 AGGODMADSMLOGSRGLTDQAIFYATPLPMPCHLVAVCPIPAAGLDVTPCGDCGTIO 1140
| | | | |
Db 1081 AGGODMADSMLOGSRGLTDQAIFYATPLPMPCHLVAVCPIPAAGLDVTPCGDCGTIO 1140
QY 1141 ENNVCLSCYQYCGRYINGHMLQHHGNSGHPVLVSYDLSAMCYCQAVYHHQALLDVKN 1200
| | | | |
Db 1141 ENNVCLSCYQYCGRYINGHMLQHHGNSGHPVLVSYDLSAMCYCQAVYHHQALLDVKN 1200
QY 1201 IAHONKRGEDMPHPH 1215
| | | | |
Db 1201 IAHONKRGEDMPHPH 1215

RESULT 4
US-09-817-538-11
; Sequence 11, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:

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; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; TITLE OF INVENTION: Deacetylase Isoforms
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1215
; TYPE: prt
; ORGANISM: Human
; US-09-817-538-11

Query Match      99.7%; Score 6375; DB 10; Length 1215;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1206; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY      1 MTSTGDSSTTRQRRSRKONPOSPPODSSVTSKRNIKGAVPSPINLAEVKKKKKKKXG 60
DB      1 MTSTGDSSTTRQRRSRKONPOSPPODSSVTSKRNIKGAVPSPINLAEVKKKKKKKXG 60
QY      61 QAMEEDLVGLGMDLNEALAGTGLVLDLQNLNFDLMDSPFEGEERLHAKEQL 120
DB      61 QAMEEDLVGLGMDLNEALAGTGLVLDLQNLNFDLMDSPFEGEERLHAKEQL 120
QY      121 QEGILDRCSVQFQAREKEELMLVHSLEYIDLMETTYQVNNEGELRYLAATYDSVYLHPS 180
DB      121 QEGILDRCSVQFQAREKEELMLVHSLEYIDLMETTYQVNNEGELRYLAATYDSVYLHPS 180
QY      121 QEGILDRCSVQFQAREKEELMLVHSLEYIDLMETTYQVNNEGELRYLAATYDSVYLHPS 180
DB      121 QEGILDRCSVQFQAREKEELMLVHSLEYIDLMETTYQVNNEGELRYLAATYDSVYLHPS 180
QY      181 YSCACLAGSVLRVDAVLAIEIRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQ 240
DB      181 YSCACLAGSVLRVDAVLAIEIRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQ 240
QY      181 YSCACLAGSVLRVDAVLAIEIRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQ 240
DB      181 YSCACLAGSVLRVDAVLAIEIRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQ 240
QY      241 KHRIRRVLIYMDVHHGGTQFTPODPSVLYFSTRYQGRFWPLKASNMSTTFGGG 300
DB      241 KHRIRRVLIYMDVHHGGTQFTPODPSVLYFSTRYQGRFWPLKASNMSTTFGGG 300
QY      241 KHRIRRVLIYMDVHHGGTQFTPODPSVLYFSTRYQGRFWPLKASNMSTTFGGG 300
DB      241 KHRIRRVLIYMDVHHGGTQFTPODPSVLYFSTRYQGRFWPLKASNMSTTFGGG 300
QY      301 QGYTINVMQVGMADADYIAAFVLYLPALEFOPOLVVAAGFDALOGDPKGEAAATP 360
DB      301 QGYTINVMQVGMADADYIAAFVLYLPALEFOPOLVVAAGFDALOGDPKGEAAATP 360
QY      301 QGYTINVMQVGMADADYIAAFVLYLPALEFOPOLVVAAGFDALOGDPKGEAAATP 360
DB      301 QGYTINVMQVGMADADYIAAFVLYLPALEFOPOLVVAAGFDALOGDPKGEAAATP 360
QY      361 AGFAQLTHLMGLAGKLLLSLEGYNLRALAEVYASLHTLLGDCPMLSESGAPCRSA 420
DB      361 AGFAQLTHLMGLAGKLLLSLEGYNLRALAEVYASLHTLLGDCPMLSESGAPCRSA 420
QY      361 AGFAQLTHLMGLAGKLLLSLEGYNLRALAEVYASLHTLLGDCPMLSESGAPCRSA 420
DB      361 AGFAQLTHLMGLAGKLLLSLEGYNLRALAEVYASLHTLLGDCPMLSESGAPCRSA 420
QY      421 QASVSCALEALEPEFVLYRSTETVYERDMEDNVESEEEGPRWEPVLPILTWPYLSR 480
DB      421 QASVSCALEALEPEFVLYRSTETVYERDMEDNVESEEEGPRWEPVLPILTWPYLSR 480
QY      421 QASVSCALEALEPEFVLYRSTETVYERDMEDNVESEEEGPRWEPVLPILTWPYLSR 480
DB      421 QASVSCALEALEPEFVLYRSTETVYERDMEDNVESEEEGPRWEPVLPILTWPYLSR 480
QY      481 TGLVYDDMMNHNCNMDSHHPVORILRMCRLEELIAGAGCLTTPPATAEALLTCH 540
DB      481 TGLVYDDMMNHNCNMDSHHPVORILRMCRLEELIAGAGCLTTPPATAEALLTCH 540
QY      481 TGLVYDDMMNHNCNMDSHHPVORILRMCRLEELIAGAGCLTTPPATAEALLTCH 540
DB      481 TGLVYDDMMNHNCNMDSHHPVORILRMCRLEELIAGAGCLTTPPATAEALLTCH 540
QY      541 SAEYVGHILRATEKMTRELHRESSNFDSIYICPSFACQALNTGAACRLVEAVISEVIN 600
DB      541 SAEYVGHILRATEKMTRELHRESSNFDSIYICPSFACQALNTGAACRLVEAVISEVIN 600
QY      541 SAEYVGHILRATEKMTRELHRESSNFDSIYICPSFACQALNTGAACRLVEAVISEVIN 600
DB      541 SAEYVGHILRATEKMTRELHRESSNFDSIYICPSFACQALNTGAACRLVEAVISEVIN 600
QY      601 GAAYVRPPGHAEADACGCFEFSNVAAARHAQTISGHALRILIVMDVHHNGTQHF 660
DB      601 GAAYVRPPGHAEADACGCFEFSNVAAARHAQTISGHALRILIVMDVHHNGTQHF 660
QY      601 GAAYVRPPGHAEADACGCFEFSNVAAARHAQTISGHALRILIVMDVHHNGTQHF 660
DB      601 GAAYVRPPGHAEADACGCFEFSNVAAARHAQTISGHALRILIVMDVHHNGTQHF 660
QY      661 EDDSVLYVSLHRXDHGTFFPWGDGASQIGRAAGTGTTVVANNGPMDADYLAANH 720
DB      661 EDDSVLYVSLHRXDHGTFFPWGDGASQIGRAAGTGTTVVANNGPMDADYLAANH 720
QY      661 EDDSVLYVSLHRXDHGTFFPWGDGASQIGRAAGTGTTVVANNGPMDADYLAANH 720
DB      661 EDDSVLYVSLHRXDHGTFFPWGDGASQIGRAAGTGTTVVANNGPMDADYLAANH 720
QY      721 RLVPVIAEFNPELVLSAGFDAAAGDPLAGGCVSPREGAHLTHLMGLASRIILILEG 780
DB      721 RLVPVIAEFNPELVLSAGFDAAAGDPLAGGCVSPREGAHLTHLMGLASRIILILEG 780
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QY      781 GYNLTISSEMACTRSILDDPPPLTLPRPPLSGALASTITETQVRRRYRSIRYAKVE 840
DB      781 GYNLTISSEMACTRSILDDPPPLTLPRPPLSGALASTITETQVRRRYRSIRYAKVE 840
QY      841 DRGPSSSKLYTKKAPAPKAPRLAERMTREKYLEAGMKVTSASGSEESTPGQTNSET 900
DB      841 DRGPSSSKLYTKKAPAPKAPRLAERMTREKYLEAGMKVTSASGSEESTPGQTNSET 900
QY      841 DRGPSSSKLYTKKAPAPKAPRLAERMTREKYLEAGMKVTSASGSEESTPGQTNSET 900
DB      841 DRGPSSSKLYTKKAPAPKAPRLAERMTREKYLEAGMKVTSASGSEESTPGQTNSET 900
QY      901 AVVALTQDOPSEATAGATLAQTISEAIGAMLGOTTSEAVAGATPDQTTSEETVGA 960
DB      901 AVVALTQDOPSEATAGATLAQTISEAIGAMLGOTTSEAVAGATPDQTTSEETVGA 960
QY      901 AVVALTQDOPSEATAGATLAQTISEAIGAMLGOTTSEAVAGATPDQTTSEETVGA 960
DB      901 AVVALTQDOPSEATAGATLAQTISEAIGAMLGOTTSEAVAGATPDQTTSEETVGA 960
QY      961 ILDTQTSSEDAVGATLAQTISEAVAGATLAQTISEAIGAMLGOTTSEAVAGATPDQTTSEETVGA 1020
DB      961 ILDTQTSSEDAVGATLAQTISEAVAGATLAQTISEAIGAMLGOTTSEAVAGATPDQTTSEETVGA 1020
QY      961 ILDTQTSSEDAVGATLAQTISEAVAGATLAQTISEAIGAMLGOTTSEAVAGATPDQTTSEETVGA 1020
DB      961 ILDTQTSSEDAVGATLAQTISEAVAGATLAQTISEAIGAMLGOTTSEAVAGATPDQTTSEETVGA 1020
QY      1021 TPPLASSTHOTPTSPVQGTTPQISPTLIGSLRTLELSESGQASQASQAPGENMLGEA 1080
DB      1021 TPPLASSTHOTPTSPVQGTTPQISPTLIGSLRTLELSESGQASQASQAPGENMLGEA 1080
QY      1021 TPPLASSTHOTPTSPVQGTTPQISPTLIGSLRTLELSESGQASQASQAPGENMLGEA 1080
DB      1021 TPPLASSTHOTPTSPVQGTTPQISPTLIGSLRTLELSESGQASQASQAPGENMLGEA 1080
QY      1081 AGGQMDADSMIMOGSRGLDQALFYAVTLPKCPHLVAVCPIPAAGLDVTPQPCGDCGTIQ 1140
DB      1081 AGGQMDADSMIMOGSRGLDQALFYAVTLPKCPHLVAVCPIPAAGLDVTPQPCGDCGTIQ 1140
QY      1141 ENNVCLSCYQVYGGRYNGHMLQHGSHRPVLYSTDLAMCYCCAYYHQAHLDPYKN 1200
DB      1141 ENNVCLSCYQVYGGRYNGHMLQHGSHRPVLYSTDLAMCYCCAYYHQAHLDPYKN 1200
QY      1201 IAHQNKFGEDMPAPH 1215
DB      1201 IAHQNKFGEDMPAPH 1215

RESULT 5
US-09-976-280A-2
; Sequence 2, Application US/09976280A
; Patent No. US20020115177A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhimin
; TITLE OF INVENTION: Regulation of Human Histone Deacetylase
; FILE REFERENCE: 004974.00590
; CURRENT APPLICATION NUMBER: US/09/976,280A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,928
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-976-280A-2

Query Match      17.6%; Score 1125; DB 10; Length 673;
Best Local Similarity 37.2%; Pred. No. 5,4e-71;
Matches 283; Conservative 89; Mismatches 225; Indels 164; Gaps 20;

QY      85 GGTGLVDEDLNEFHCLMDSPF---EGPERLHAKEQLQELDLRCVSFQAREKEE 140
DB      2 GATLVYHEDMTATRLMD--PCETETPERLHAKEQLQELDLRCVSFQAREKEE 59
QY      141 LMLVHSLEYIDLMETTYQVNNEGELRYLAATYDSVYLHPSYSCACLAGSVLRVDAVLA 200
DB      60 LGLVHSPEYVSLVREHGVGKEQLQSLGQFQALYFHPSTFHCAKRLAAGGLDLYDAVLT 119
QY      201 AETRNGMALIRPPGHHQSHLMDGYCMFNHVAAYAAQKHIRRVLYMDVHHNGT 260
DB      120 GAVONGLALVVRPPGHGQRAANGFCVFNNVLAIAAHAKQKJELRILIVMDVHHNGT 179
QY      261 QFTPODPSVLYFSTRYQGRFWPLKASNMSTTFGGGQGTINVMQVGMADADY 320
DB      180 QTLFEDPSVLYFSTRYQGRFWPLKASNMSTTFGGGQGTINVMQVGMADADY 239
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Query Match	12.6%	Score 805.5;	DB 9;	Length 1084;
Best Local Similarity	46.0%;	Pred. No. 4.1e-48;		
Matches 185; Conservative	54;	Mismatches 118;	Indels 45;	Gaps 12

RESULT 9
US-10-173-539-12

Sequence 12, Application US/10173539
Publication No. US20030059812A1
GENERAL INFORMATION:
APPLICANT: Richon, Victoria
APPLICANT: Zhou, Xiabo
APPLICANT: Rickind, Richard A.
APPLICANT: Marks, Paul A.
TITLE OF INVENTION: HNA9 Polypeptides and Polynucleotides
FILE REFERENCE: 3254.1000-003
CURRENT APPLICATION NUMBER: US/10/173,539
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/298,173
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/311,686

Query Match	12.6%	Score 805.5;	DB 9;	Length 1084;
Best Local Similarity	46.0%;	Pred. No. 4.1e-48;		
Matches 185; Conservative	54;	Mismatches 118;	Indels 45;	Gaps 12

RESULT 10
US-09-817-913-7

; Sequence 7, Application US/09817913
; Patent No. US20020061860A1

```

? GENERAL INFORMATION:
? APPLICANT: Li, Zuomel
? APPLICANT: Bonfilis, Claire
? APPLICANT: Besterman, Jeffrey
? TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
? FILE REFERENCE: 106101.145
? CURRENT APPLICATION NUMBER: US/09/817,913
? CURRENT FILING DATE: 2001-03-26
? PRIOR APPLICATION NUMBER: US 60/192,157
? PRIOR FILING DATE: 2000-03-24
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 7
? LENGTH: 967
? TYPE: PRT
? ORGANISM: Human
? IS-09-817-913-7

```

Query Match	12.5%	Score 801.5	DB 10	Length 967
Best Local Similarity	45.8%	Pred. No. 6.6e-48		
Matches 184	Conservative 54	Mismatches 119	Indels 45	Gaps 12
QY	465	EPPLPILTPVLOSRTGLVYDQNNMH-CNLV-DSHHPVPRITLIMKRLLESLAGR	522	
b	528	EPPLPDRPT-----TGLVYDITLMKIKOCTGSSSHPRAGISITWRSRLDTLGRG	580	

QY 523 CULTPRPATEALLTCHSAEYVGHILRATEKKTREHRE-----SSNF-----566
 DB 581 CECIRGRKATLEELQTYHSEAHF-LTYGNPLNRKLDKSKLLGSLASVYFVRLPCGGVGV 639
 QY 567 --DSIYICPSTFACQALATGACRLVEAVLSEGVINGAIVRPPGHHAEDDAACGFCFEN 624
 DB 640 DSDTIWNEVHSGAARLAVGVVELVFKVATGELKNGRVAVRPPGHHAEDSTPMGFCYFN 699
 QY 625 SVAVAARHAQ--TISGHALRILYDMVHNHNGTQHMEDDPVLYVSLHRYDHGTFFP 681
 DB 700 SVAVAARKILQORLSYS----KILYDMVHNHNGTQOAFYSDPSVLYMSLHRYDGNFPP 755
 QY 682 MGDGASSQIGRAAGTGTNNVAMNG---PRMGADYLAAMRVLPLAYEENPELVYVS 738
 DB 756 --GSGAPDEVGTGPGGVNMAFTGGDPPMGDAEYLAARFTVMPPIASEFAPDVYLAS 813
 QY 739 AGFDAARG--DPLGGCOVSPEGYAHILTHLMGLASGRITLLEGGVNLTSISESMAACTR 796
 DB 814 SGFDVAEGHPTPLGGVNLASRCFGLTKQMLAGRLVLALEGGHDLTAICDASEACVS 873
 QY 797 SLIG--DPPLLTLPRPLSGALASITETIOVHRRYRSLSR 835
 DB 874 ALLGNEIDPLPEKYLQQRPNANAVRSMKMEIHSKYRCLQ 915

RESULT 11

US-09-817-538-7
 ; Sequence 7, Application US/09817538
 ; Patent No. US20020137162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Zuomei
 ; APPLICANT: Bonfils, Claire
 ; APPLICANT: Besterman, Jeffrey
 ; TITLE OF INVENTION: Antisense oligonucleotide inhibition of Specific Histone
 ; FILE REFERENCE: 106101.144
 ; CURRENT APPLICATION NUMBER: US/09/817.538
 ; CURRENT FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: US 60/192.157
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 967
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-817-538-7

Query Match 12.5%; Score 801.5; DB 10; Length 967;
 Best Local Similarity 45.8%; Pred. No. 6.6e-48;
 Matches 184; Conservative 54; Mismatches 119; Indels 45; Gaps 12;

QY 465 EPPVLPILTWPVYLSRGVLYDQMANH-CNLM-DSHPEVPORILIMCRLEELAGLR 522
 DB 528 EPPKPPPT-----TGLVYDTLMLKHCQTCGSSSHPEHARIGQISIMSRLOETGRK 580
 QY 523 CULTPRPATEALLTCHSAEYVGHILRATEKKTREHRE-----SSNF-----566
 DB 581 CECIRGRKATLEELQTYHSEAHF-LTYGNPLNRKLDKSKLLGSLASVYFVRLPCGGVGV 639
 QY 567 --DSIYICPSTFACQALATGACRLVEAVLSEGVINGAIVRPPGHHAEDDAACGFCFEN 624
 DB 640 DSDTIWNEVHSGAARLAVGVVELVFKVATGELKNGRVAVRPPGHHAEDSTPMGFCYFN 699
 QY 625 SVAVAARHAQ--TISGHALRILYDMVHNHNGTQHMEDDPVLYVSLHRYDHGTFFP 681
 DB 700 SVAVAARKILQORLSYS----KILYDMVHNHNGTQOAFYSDPSVLYMSLHRYDGNFPP 755
 QY 682 MGDGASSQIGRAAGTGTNNVAMNG---PRMGADYLAAMRVLPLAYEENPELVYVS 738
 DB 756 --GSGAPDEVGTGPGGVNMAFTGGDPPMGDAEYLAARFTVMPPIASEFAPDVYLAS 813

QY 739 AGFDAARG--DPLGGCOVSPEGYAHILTHLMGLASGRITLLEGGVNLTSISESMAACTR 796
 DB 814 SGFDVAEGHPTPLGGVNLASRCFGLTKQMLAGRLVLALEGGHDLTAICDASEACVS 873
 QY 797 SLIG--DPPLLTLPRPLSGALASITETIOVHRRYRSLSR 835
 DB 874 ALLGNEIDPLPEKYLQQRPNANAVRSMKMEIHSKYRCLQ 915

RESULT 12

US-10-072-094-6
 ; Sequence 6, Application US/10072094
 ; Publication No. US2003002538A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JACKSON, DONALD
 ; APPLICANT: LORENZI, MATTHEW
 ; APPLICANT: ATTAR, RICARDO
 ; APPLICANT: GOTTARDIS, MARCO
 ; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
 ; FILE REFERENCE: 3053-4145US1
 ; CURRENT APPLICATION NUMBER: US/10/072.094
 ; CURRENT FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: 60/298.296
 ; PRIOR FILING DATE: 2001-06-14
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 706
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-10-072-094-6

Query Match 12.3%; Score 788; DB 9; Length 706;
 Best Local Similarity 35.4%; Pred. No. 3.7e-47;
 Matches 180; Conservative 90; Mismatches 190; Indels 48; Gaps 12;

QY 436 EYLVNSTETVER---DNMEEDNVESEEGPWE---PVPVLPILTWPVYLSRGVLYDQMAN 489
 DB 9 EYLVNDHDLKRLKENKEBENSLSSTSKRKQVIVPCPKIHYSP--KTGICGVYRM 66
 QY 490 MNHCNIMDSH-----HPEVPORILIMCRLEELG-----LAGRCILTPRPA 531
 DB 67 RYHAKIFTSYFEYIDHPEDPRIRIYKILANGILNDPTLSGVLDGLMLKIPYRAA 126
 QY 532 TEAEILTCHSAEYVGHILRATEKKTREHRESNPSIYICPSTFACQALATGACRLVE 591
 DB 127 TSEELLEVHTKELEFTESTEKMSREELKETEKGDSVYFNDSYASARLPCGAIACK 186
 QY 592 AVLSGEVLNGAIVRPPGHHAEDDAACGFCFENSVAVAARH-AOTISGHALRILYDMV 650
 DB 187 AVYEGSVKNSLAVVRPPGHHAEDQAAGGFCLESNVAANKIINKNPESTRILIMLMDI 246
 QY 651 HHNGTQHMEDDPVLYVSLHRYDHGTFFPMGDEGASSQIGRAAGTGTNNVAMNGPRM 710
 DB 247 HHNGTQKSFYQDDQVLYVSLHREFEMGKTYPGTIGQYDQGTGSKGFGFNCNITWPGGV 306
 QY 711 GPADYLAAMRVLPLAYEENPELVYSAFGDAARDPLAGGCOVSPGYAHILTHLMGLA 770
 DB 307 GDAEYMAAEQVYMPMGREFKPDVLISSGFGDAADDITIGQCHVTSPCYGHMTHMLKSLA 366
 QY 771 SGRIILILEGGVNLTSISESMAACTRSILGDDPPLTLPRP---PLSGALASTETIOVH 827
 DB 367 RGNLCVLEEGSINTDAIASALSAVAVLIGEPD--ELDPDLSDPREYEMIDKATRLQ 424
 QY 828 RRYWSRLRYMKE---DREGPSSSKLVTKAPQAPAKPRLAERMTEKKVLEAGMGKVT- 883
 DB 425 SKYWCFFRRRHNASGCFNEPINDSIISKNF-----LQKATRQOQOHYLSOEFNVTL 478
 QY 884 ---SASFGEES---TPGQJNSETAVAYAL 905
 DB 479 PLVSMIDLPTNVLCTPNISESNTIIVV 506

RESULT 13
US-09-563-728A-32
; Sequence 32, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; NUMBER OF SEQ ID NOS: 1999-05-03
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 716
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-728A-32

Query Match 12.2%; Score 778.5; DB 9; Length 716;
Best Local Similarity 37.1%; Pred. No. 1.8e-46;
Matches 192; Conservative 79; Mismatches 179; Indels 67; Gaps 16;
QY 408 PLESPGAPCRSAQASVSCALELEPFEVLYVSTVEYERDNMEDNVESEBEGPWEPP 467
DB 211 PLEBPGAGYKLLFSDAQ-PLQPLQYQAPL-SLATVPHQALGRTOSSPAAPGKMSPP 267
QY 468 VLPI--LTWPVLQSRGTGLVYDQNMNH-CNLMDSH-HPEVPOKILRIMCRLEELAGR 522
DB 268 DQPKHLFT-----TGVYDTFMLKHQCMGNTFHPHAGRIQSIWSRLDETGLSK 320
QY 523 CLITLPPRPAEALLTCHSAEYVGHRLATEKMKTRLEHRE-----S 563
DB 321 CERIRGRKATIDEIQTVHS-EYHTLLYGTSPLNROKIDSKLLGPISOKMYAVLPCCGIG 379
QY 564 SNFDSIYICPSTFCAQALTGACRLVEAVLSGEVLYNGAAYVRRPGHHAEDDAGCGCF 623
DB 360 VDSIDVYWNEMHSSSAVMAVAGCLLEAFKVAAGELKNGFALLRPHGHAESTAMGCF 439
QY 624 NSVAVAARHAQOTISGHARILLVDMVHNGNGTOHMEEDPSVLYVSLHRYDGTFFPMG 683
DB 440 NSVAITAKLLQ-KLVNGKVLIVDMDIHNGNGTOQAFYNDPSVLYISLHRYDNGNFP 496
QY 684 DEGASSOIGRAAGTGFYVNAVNG--PRMGADYLAAMHRLVLPATYEPNPELVYSAG 740
DB 497 GSGAPEEYGGPGVGVYNAVMTGVDPRIGDVEYLTAFRTVMPFAHFEFSPDVLVSAG 556
QY 741 FDAARG--DPLGCGOVSPGEGYAHLLHLMGLASGRILLLEGYNLTISSEMAACTRSL 798
DB 557 FDAVGHLSPLGIGYVTAFCFGLTRQMLTLAGGRVLLAEGGHDLTALCDASEACVSAL 616
QY 799 LG---DPPPLLLPRPPLSGALASITETIQVHRRY-----RSLR--YAKVED 841
DB 617 LSELQPLDEAVLQOKPKNINAVATLEKVEIQSKHMSCVQKFAAGLSRLRAGAGTTEE 676
QY 842 REGPSSSKLYTKKAPQPA-----KPLAERMTRRE 871
DB 677 AETVSAMALLSVGAEOAQAARHSRPRAEPEMEOE 713

RESULT 14
US-10-072-094-8
; Sequence 8, Application US/10072094
; Publication No. US20030025538A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES

; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-094-8

Query Match 12.2%; Score 778.5; DB 9; Length 1122;
Best Local Similarity 37.1%; Pred. No. 3.5e-46;
Matches 192; Conservative 79; Mismatches 179; Indels 67; Gaps 16;
QY 408 PLESPGAPCRSAQASVSCALELEPFEVLYVSTVEYERDNMEDNVESEBEGPWEPP 467
DB 617 PLEBPGAGYKLLFSDAQ-PLQPLQYQAPL-SLATVPHQALGRTOSSPAAPGKMSPP 673
QY 468 VLPI--LTWPVLQSRGTGLVYDQNMNH-CNLMDSH-HPEVPOKILRIMCRLEELAGR 522
DB 674 DQPKHLFT-----TGVYDTFMLKHQCMGNTFHPHAGRIQSIWSRLDETGLSK 726
QY 523 CLITLPPRPAEALLTCHSAEYVGHRLATEKMKTRLEHRE-----S 563
DB 727 CERIRGRKATIDEIQTVHS-EYHTLLYGTSPLNROKIDSKLLGPISOKMYAVLPCCGIG 785
QY 564 SNFDSIYICPSTFCAQALTGACRLVEAVLSGEVLYNGAAYVRRPGHHAEDDAGCGCF 623
DB 786 VDSIDVYWNEMHSSSAVMAVAGCLLEAFKVAAGELKNGFALLRPHGHAESTAMGCF 845
QY 624 NSVAVAARHAQOTISGHARILLVDMVHNGNGTOHMEEDPSVLYVSLHRYDGTFFPMG 683
DB 846 NSVAITAKLLQ-KLVNGKVLIVDMDIHNGNGTOQAFYNDPSVLYISLHRYDNGNFP 902
QY 684 DEGASSOIGRAAGTGFYVNAVNG--PRMGADYLAAMHRLVLPATYEPNPELVYSAG 740
DB 903 GSGAPEEYGGPGVGVYNAVMTGVDPRIGDVEYLTAFRTVMPFAHFEFSPDVLVSAG 962
QY 741 FDAARG--DPLGCGOVSPGEGYAHLLHLMGLASGRILLLEGYNLTISSEMAACTRSL 798
DB 963 FDAVGHLSPLGIGYVTAFCFGLTRQMLTLAGGRVLLAEGGHDLTALCDASEACVSAL 1022
QY 799 LG---DPPPLLLPRPPLSGALASITETIQVHRRY-----RSLR--YAKVED 841
DB 1023 LSELQPLDEAVLQOKPKNINAVATLEKVEIQSKHMSCVQKFAAGLSRLRAGAGTTEE 1082
QY 842 REGPSSSKLYTKKAPQPA-----KPLAERMTRRE 871
DB 1083 AETVSAMALLSVGAEOAQAARHSRPRAEPEMEOE 1119

RESULT 15
US-10-072-094-91
; Sequence 91, Application US/10072094
; Publication No. US20030025538A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 1122

! TYPE: PRT
! ORGANISM: Homo sapiens
US-10-072-094-91

Query Match 12.2%; Score 778.5; DB 9; Length 1122;
Best Local Similarity 37.1%; Pred. No. 3.5e-46;
Matches 192; Conservative 79; Mismatches 179; Indels 67; Gaps 16;

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QY 408 PMLESPAGPCSAASQASVSCALELEFEWEVLYRSTETVERDNMEEDNVESEEGPWEP 467
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 617 PDLEEPGAGYKKLPDSAQ-PLQPLQVYQAPL--SLATVPHQATGRTQSSPAAGCKSP 673
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 468 VLPI--LTPVLSRGLVYDQMMNH-CNLMDSH-HPEVQRILRMCRLEELAGLR 522
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 674 DQPKHLEF-----TGVTDTFMKHKQCMGNTVHPEHAGRIQSIWSRLQETGLSK 726
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 523 CLATLPPRPAEALLTCHSAEYVGHLRATEKKTRELRE-----S 563
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 727 CERIRGRKATLDEIQTVHS-EYHLLVGTSPLNROKLDKSLGPIISQKMYAVLPQGGIG 785
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 564 SNPDSIITICSTFACQALGACRLYEAVLSGEVLNGAAYVRPGHHAEDDAGCGFCF 623
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 786 VDSDTVMNEMHSSAVPMAYVCLLELAFKVAAGELKNGFALIRPGHHAESTAMGFCF 845
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 624 NSVAVARHQAOTISGHALRIIYDMDVHNGTQHMEDDPSVLYSLHRIDHGTFFPMG 683
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 846 NSVAITAKLLQO-KLNVGKVLIVDMDIHNGTQOAFYNDPSVLYSLHRYDNGNFP-- 902
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 684 DEGASSQIGRAAGTFTVNVAMNG--PRMGDADYLAAMHRLVPLIAYEFNPELVLSAG 740
    || : : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 903 GSGAPEEVGGPGVGVNVNVAMTGVDPPIGDVEYLTAFRTVMPFAHEFSPDVVLSAG 962
    || : : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 741 FDAARG--DPLGGQVSPGYAHLTHLMGLASGRILLLEGYNLTSSISMAACTRSL 798
    ||| | : : | : | : | : | : | : | : | : | : | : | : | : | :
DB 963 FDAVEGHLSPLIGSYTARCGHLTRQMLTAGGRVYALLEGHDLFAICDASEACYSAL 1022
    ||| | : : | : | : | : | : | : | : | : | : | : | : | : | :
QY 799 LG--DPPPLTLPRPLSGMLASITETIOVHRRW-----RSLR--VMKYED 841
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 1023 LSYELQPLDEAVLQOKPNNVATLEKVIETIOSKHWSCVQKFAAGLGRSLREAQAGETEE 1082
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 842 REGPSSSKLVYTKKAPPA-----KPLAERMTTRE 871
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 1083 AETVSAVALLSVGAEOQAQAAAAAREHSPRAPEPMEOE 1119
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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Search completed: June 6, 2003, 14:58:56
Job time : 59 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 16:37:51 ; Search time 752 Seconds
(without alignments)
10924.588 Million cell updates/sec

Title: US-09-800-187-5

Perfect score: 3648
Sequence: 1 atgacctcaacgcgcagga.....atagcccccacacactaa 3648

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
N.Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
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7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3646.4	100.0	6949	24	AAS95017	Human DNA sequence
2	3612.4	99.0	4099	24	ABR87720	Human CDNA encodin
3	2282	62.6	2552	22	AAH18350	Human CDNA sequenc
4	2182.6	59.8	2548	22	AAH14416	Human CDNA sequenc
5	1398.8	38.3	2107	21	AAC59704	Human secreted pro
6	628.2	17.2	638	22	AAH06343	Human CDNA clone (
7	602.2	16.5	743	22	AAH03528	Human CDNA clone (
8	453.2	12.4	4689	23	ABH10649	Drosophila melanog
9	398.4	10.9	424	20	AAV87399	EST clone CD146.

10	347.6	9.5	2461	21	AAC76966	Human ORFX ORF2521
11	346	9.5	2022	24	ABO73028	Human HDAC9 encodi
12	346	9.5	2022	24	ABD36979	Human histone deac
13	346	9.5	2104	24	ABO73030	Human HDAC9 varian
14	346	9.5	2480	21	AAC76952	Human ORFX ORF2507
15	325.8	8.9	1005	22	AAAS4280	CDNA encoding nove
16	300.6	8.2	9384	22	ABH10648	Drosophila melanog
17	289.8	7.9	1129	24	ABO73027	Human HDAC9 ORF nu
18	278.2	7.6	744	24	ABO73013	Human HDAC9 relate
19	235.4	6.5	2621	21	AAH81740	Human secreted pro
20	229.6	6.3	1875	21	ABO73031	Human HDAC9 varian
21	215.4	5.9	1725	21	AAAS1856	Caspase 8-Interact
22	215.4	5.9	4200	22	AAK53008	Human polynucleoti
23	215.4	5.9	4245	22	AAK53024	Human polynucleoti
24	215	5.9	2430	22	ABH90159	Human CDNA sequenc
25	213.8	5.9	3208	22	AAH14008	Human ORFX ORF2609
26	213.8	5.9	4189	21	AAH77054	Human CDNA encodin
27	208.6	5.7	3131	24	ABK87721	Human CDNA sequenc
28	204.4	5.6	2026	22	AAH13829	Human CDNA encodin
29	201	5.5	606	22	AAH03697	Human CDNA clone (
30	194	5.3	8459	22	AAC89557	Human histone deac
31	192.4	5.3	8460	22	ABK87718	Human CDNA encodin
32	175.2	4.8	4021	21	AAC77217	Human ORFX ORF2772
33	173.6	4.8	2233	22	AAC89558	Human histone deac
34	173.6	4.8	2233	24	ABK87719	Human CDNA encodin
35	173.6	4.8	2885	20	AAH40055	Human CDNA encodin
36	170.8	4.7	2205	24	ABO73029	Human HDAC9 relate
37	165.8	4.5	1355	24	ABK34632	Human HDAC9 relate
38	163	4.5	719	22	AAH07464	Human CDNA clone (
39	161.4	4.4	1880	22	AAH16517	Human CDNA sequenc
40	160.8	4.4	843	24	ABO73009	Human CDNA sequenc
41	158	4.3	3894	23	ABH03353	Human HDAC9 relate
42	142	3.9	560	22	AAH11402	Drosophila melanog
43	140.4	3.8	1452	22	AAH62798	Human CDNA clone (
44	139.6	3.8	631	24	ABO73018	CDNA sequence #585
45	139.2	3.8	1991	21	AAC34680	Human HDAC9 relate
						Arabidopsis thailia

ALIGNMENTS

RESULT 1	
AAS95017/c	
ID AAS95017 standard; DNA: 6949 BP.	
XX AC AAS95017;	
XX AC	
DT 14-FEB-2002 (first entry)	
XX XX	
DE Human DNA sequence #272 expressed during foam cell differentiation.	
XX XX	
KW Human; foam cell differentiation; atherosclerosis; cerebral stroke;	
KW Cardiovascular disorder; coronary artery disease; gene therapy; ds.	
XX XX	
OS Homo sapiens.	
XX XX	
PN W0200177389-A2.	
XX XX	
PD 18-OCT-2001.	
XX XX	
PF 04-APR-2001; 2001WO-US11128.	
XX XX	
PR 05-APR-2000; 2000US-195106P.	
XX XX	
PA (INCY-) INCYTE GENOMICS INC.	
XX XX	
PI Shiffman D, Somogyi R, Lawn R, Sellhammer JU, Porter GJ, Mikita T;	
PI Tal J;	
XX XX	
DR WPI; 2002-010925/01.	
XX XX	
PT Composition useful for diagnosis of conditions, disorders or diseases	
PT associated with atherosclerosis, comprises several polynucleotides that	

D	5019	GGTGTCTGCTGTGGTGTGCTCCCCAGCACACCAACCAGAAACAAGATGAAGAATTCCGGTTT	4960
OY	1861	TGCTTTTTCACCTCTGTGGCTGTGGCTGCCTGCCAATGGCCAGACTATCAGTGGGATGCC	1920
D	4959	TGCTTTTTCACCTCTGTGGCTGTGGCTGCCTGCCAATGGCCAGACTATCAGTGGGATGCC	4900
OY	1921	CACGGATCTCGATTTGTGGATTGGGATGTCCACCAAGGTAAATGAACCTCAGACATGTTT	1980
D	4899	CTACGGATCTCGATTTGTGGATTGGGATGTCCACCAAGGTAAATGAACCTCAGACATGTTT	4840
OY	1981	GAGGATGACCCAGTGCTGTATATGTGTCCCTGACACCGCTATGATCATGGCACTTCTTC	2040
D	4839	GAGGATGACCCAGTGCTGTATATGTGTCCCTGACACCGCTATGATCATGGCACTTCTTC	4780
OY	2041	CCCATGGGGGATGAGGGTCCACGACGACGATGGGCGGGGCTGGGGGACAGGGCTTCAC	2100
D	4779	CCCATGGGGGATGAGGGTCCACGACGACGATGGGCGGGGCTGGGGGACAGGGCTTCAC	4720
OY	2101	GTCAACGTGGCATGGAAGGGGCCCCGCAATGGGTGATGTCACTACCTAGTCCCGCAT	2160
D	4719	GTCAACGTGGCATGGAAGGGGCCCCGCAATGGGTGATGTCACTACCTAGTCCCGCAT	4660
OY	2161	CGCGGTGCTCCCATTTGCGCTACGAGTTTAACCCAGAACGTGTCTGTCTCAGCTGGC	2220
D	4659	CGCGGTGCTCCCATTTGCGCTACGAGTTTAACCCAGAACGTGTCTGTCTCAGCTGGC	4600
OY	2221	TTTTGATGCTGACAGGGGGGATCCGTGGGGGGCTCCAGAGTGTCACCTGAGAGGTATGCC	2280
D	4599	TTTTGATGCTGACAGGGGGGATCCGTGGGGGGCTCCAGAGTGTCACCTGAGAGGTATGCC	4540
OY	2281	CACCTCACCCACTCTGATATGGGCTTGCCACAGTGGCCGCAATATCCTATCTCTAGAGGT	2340
D	4539	CACCTCACCCACTCTGATATGGGCTTGCCACAGTGGCCGCAATATCCTATCTCTAGAGGT	4480
OY	2341	GGCTTAACCTGACATCCATCTCABAAGTCCATGGTGGCTGCATCTGCCTCCTCTTGA	2400
D	4479	GGCTTAACCTGACATCCATCTCABAAGTCCATGGTGGCTGCATCTGCCTCCTCTTGA	4420
OY	2401	GACCCACCAACCCCTCTGACCTGGCCAGCGCCCCCAATGAGGGGCCCTGGCCCATC	2460
D	4419	GACCCACCAACCCCTCTGACCTGGCCAGCGCCCCCAATGAGGGGCCCTGGCCCATC	4360
OY	2461	ACTGAGACCATCCAAGTCCATGCGACAGATCTGGCGCAGCTTACGGGTCATGAAGTAGAA	2520
D	4359	ACTGAGACCATCCAAGTCCATGCGACAGATCTGGCGCAGCTTACGGGTCATGAAGTAGAA	4300
OY	2521	GACAGAGAAGACCCCTCCAGTCTTAAGTGTGGTCCACCAAAGGACCCCAACGCCAAA	2580
D	4329	GACAGAGAAGACCCCTCCAGTCTTAAGTGTGGTCCACCAAAGGACCCCAACGCCAAA	4240
OY	2581	CCTAGGTTAGCTGAGCGGATGACCAAGAAAAAAGGTTTCTGGAAGCGGATGAGGG	2640
D	4239	CCTAGGTTAGCTGAGCGGATGACCAAGAAAAAAGGTTTCTGGAAGCGGATGAGGG	4180
OY	2641	AAAGTCACCTGGCATCTTTGGGGAGAGTCCACTCCAGGCCAGACTAACTCAGAGACA	2700
D	4179	AAAGTCACCTGGCATCTTTGGGGAGAGTCCACTCCAGGCCAGACTAACTCAGAGACA	4120
OY	2701	GCTGGTGGGCGCCTCAGGACGAGGCCCTCBAAGGACGACCAAGGGGGAGCCACTCTG	2760
D	4119	GCTGGTGGGCGCCTCAGGACGAGGCCCTCBAAGGACGACCAAGGGGGAGCCACTCTG	4060
OY	2761	GCCCAGACCAATTTCTGAGGACGACCAATTTGGGGAGGACCAATGCGGGCCAGACCACTCGAG	2820
D	4059	GCCCAGACCAATTTCTGAGGACGACCAATTTGGGGAGGACCAATGCGGGCCAGACCACTCGAG	4000
OY	2821	GAGGCTGTGCGGGGAGCCACTCCGGAACAGACCACTCAAGAGAGACTGTGGAGAGACC	2880
D	3999	GAGGCTGTGCGGGGAGCCACTCCGGAACAGACCACTCAAGAGAGACTGTGGAGAGACC	3940
OY	2881	AATTGAGACAGACCACTCAGAGAGATGCTTTGGGGGAGGACCAAGCGGGGCCAGACTACC	2940
D	3939	AATTGAGACAGACCACTCAGAGAGATGCTTTGGGGGAGGACCAAGCGGGGCCAGACTACC	3880

	ID	Sequence	Position
QY	2941	TCAAGGAGGGCGTGTATGGAGGACCTCACTGGGCCGACCAACTTCGTGGAGGCAGCCATGGAG	3000
Dd	3879	TGAAGGAGAGGCGTGTAAGGAGAGCACTAAGTTGGGCCAGAACCTCTGGAGGCGCATGGAG	3820
QY	3001	GGAGGCACACTGAGGACCAGACTACGTCAAGAGGAGGCGTCCAGGGGGACCGACACTGATCCA	3060
Dd	3819	GGAGGCACACTGAGGACCAGACTACGTCAAGAGGAGGCGTCCAGGGGGACCGACACTGATCCA	3760
QY	3061	ACTCCTCTTAGCCTCGACAGACAGACCACCAGAACCCCCCACTCACCTGTGTCAGAGGAAGT	3120
Dd	3759	ACTCCTCTTAGCCTCGACAGACAGACCACCAGAACCCCCCACTCACCTGTGTCAGAGGAAGT	3700
QY	3121	AACACCCAGATATCTCCCAAGTACAATGATTTGGGAGTCTCAGAGCCTTGGAGCTTACGACGC	3180
Dd	3639	ACACCCAGATATCTCCCAAGTACAATGATTTGGGAGTCTCAGAGCCTTGGAGCTTACGACGC	3640
QY	3181	GAAATCTCAGGGGGGCTTCAGAAATCTTCAGGCCCCCAGAGAGAGGAACCTACTTGGAGAGGCA	3240
Dd	3639	GAAATCTCAGGGGGGCTTCAGAAATCTTCAGGCCCCCAGAGAGAGGAACCTACTTGGAGAGGCA	3580
QY	3241	GCTGAGAGTCAAGAGATAGGCTGATTCCATGCTGATGACAGGGATCTAGGGGCTCTACTGAT	3300
Dd	3579	GCTGAGAGTCAAGAGATAGGCTGATTCCATGCTGATGACAGGGATCTAGGGGCTCTACTGAT	3520
QY	3301	CAGGCGCATATTTTATGCTGTACACACCACTGGCCGCTGTGTCCCATTGGTGGGCAGTATGC	3360
Dd	3519	CAGGCGCATATTTTATGCTGTACACACCACTGGCCGCTGTGTCCCATTGGTGGGCAGTATGC	3460
QY	3361	CCCATACCTGACAGCAGGCGCTTAGAGCTGACCCCAACCTTGGGGAGCTGGAACAATCCAA	3420
Dd	3459	CCCATACCTGACAGCAGGCGCTTAGAGCTGACCCCAACCTTGGGGAGCTGGAACAATCCAA	3400
QY	3421	GAGAAATGGGTGTCTCTCTTCTATCAGGCTTACTGTGTGCTGTACATCATATGGCCAC	3480
Dd	3399	GAGAAATGGGTGTCTCTCTTCTATCAGGCTTACTGTGTGCTGTACATCATATGGCCAC	3340
QY	3481	ATGCGCCAAACACANTGGAAATTTGGAACACCCGGTGGTCCACACTCATGACGACCTGTCA	3540
Dd	3339	ATGCGCCAAACACANTGGAAATTTGGAACACCCGGTGGTCCACACTCATGACGACCTGTCA	3280
QY	3541	GCGTGGTGTACTACTGTCAAGCCCTATGTCACACACAGAGCTCTCTAGATGTGMAAAC	3600
Dd	3279	GCGTGGTGTACTACTGTCAAGCCCTATGTCACACACAGAGCTCTCTAGATGTGMAAAC	3220
QY	3601	ATCGGCCACACGAACAAGTTGGGGAGAGATATGCCCAACCCACACTCAA 3648	
Dd	3219	ATCGGCCACACGAACAAGTTGGGGAGAGATATGCCCAACCCACACTCAA 3172	
RESULT 2			
ABK87720			
ID	ABK87720	standard; cDNA; 4099 BP.	
XX	AC	ABK87720;	
XX	DT	07-OCT-2002 (first entry)	
XX	XX		
DE	Human CDNA encoding Histone deacetylase isoform 6.		
XX	XX		
KW	Human; ss; gene; histone deacetylase; HDAC-6; cancer; cytostatic;		
KW	antisense; tumour suppressor; cell proliferation; tumour;		
KW	programmed cell death; necrotic cell death.		
XX	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
FH	CDS	94..3741	
FT		/*tag= a	
FT		/product= "HDAC-6"	
FT		/transl_except= (pos:604..606,aa:Tyr)	
FT		/transl_except= (pos:823..825,aa:Ile)	
FT		/transl_except= (pos:1093..1095,aa:Phe)	

Query Match	Best Local Similarity	Matches 3625	Conservative	0	Mismatches	23	Indels	0	Gaps	0
1	ATGACCTTCACCGCCAGATTCCACCAACACGAGGACGAGGAGGATGAGCAGAACCC	60								

Db	94	ATGACCTCAACCGGSCAGGATTCACACCAACGAGGAGGAATAGCAGAACCC	153
OY	61	CAGTCGCCCTCTGAGACTCCAGTGTACTTCCGAAAGGAATTTAAAAAGGAGCCGTT	120
Db	154	CAGTCGCCCTCTGAGACTCCAGTGTACTTCCGAAAGGAATTTAAAAAGGAGCCGTT	213
OY	121	CCCGGCTCTAATCCCACTAGCGGAGGTAAAGAAAGGCAAAATGAAAGAGCTCGG	180
Db	214	CCCGGCTCTAATCCCACTAGCGGAGGTAAAGAAAGGCAAAATGAAAGAGCTCGG	273
OY	181	CAAGCAATGGAAGAAGACTAATCGTGGAGCTCAAGGAGTGGATCGAACTTTGAGGT	240
Db	274	CAAGCAATGGAAGAAGACTAATCGTGGAGCTCAAGGAGTGGATCGAACTTTGAGGT	333
OY	241	GAACCACTGGCTGGCATTGGCTTTGGTTTGGATGAGCAGTTAAATGAATTCATTGCTTC	300
Db	334	GAACCACTGGCTGGCATTGGCTTTGGTTTGGATGAGCAGTTAAATGAATTCATTGCTTC	393
OY	301	TGGGATACAGCTTCCCGGAAGCCCTGAGCGGCTCCATCCATCAAGGAGCAACTGATC	360
Db	394	TGGGATACAGCTTCCCGGAAGCCCTGAGCGGCTCCATCCATCAAGGAGCAACTGATC	453
OY	361	CAGGAGGGCCTCCTAGATCGCTGCTGCTCTTTCAGGCCCCGTTTGTCTGAAAAGGAG	420
Db	454	CAGGAGGGCCTCCTAGATCGCTGCTGCTCTTTCAGGCCCCGTTTGTCTGAAAAGGAG	513
OY	421	CTGATGTTGGTTCACACCTAGAAATATATGATCTGATGGAACAACCCAGTCAATGAT	480
Db	514	CTGATGTTGGTTCACACCTAGAAATATATGATCTGATGGAACAACCCAGTCAATGAT	573
OY	481	GAGGAGAAACCTCGGTGCTAGACAGACCTTAGACACTCAATTATCTGATCCGAACTCA	540
Db	574	GAGGAGAAACCTCGGTGCTAGACAGACCTTAGACACTCAATTATCTGATCCGAACTCA	633
OY	541	TACTCTGTGCTGCTGAGGCTCCTGAGGCTGTGCTCAGGCTGGTGGATGGGCTCTGGGG	600
Db	634	TACTCTGTGCTGCTGAGGCTCCTGAGGCTGTGCTCAGGCTGGTGGATGGGCTCTGGGG	693
OY	601	GCTGAGATCCGGGAATGGCATAGGCATCATATGAGCCCTCGGACATACGCCCAAGCACT	660
Db	694	GCTGAGATCCGGGAATGGCATAGGCATCATATGAGCCCTCGGACATACGCCCAAGCACT	753
OY	661	CTTATGATGAGGCTATTCATGTTTCAACACAGTGGCTGGACCCCGTATGCTCAACAG	720
Db	754	CTTATGATGAGGCTATTCATGTTTCAACACAGTGGCTGGACCCCGTATGCTCAACAG	813
OY	721	AAACACCGCATCCGGAGGTCCTTATGATGATGGAATGGATGTCACACGGTCAAGGACA	780
Db	814	AAACACCGCATCCGGAGGTCCTTATGATGATGGAATGGATGTCACACGGTCAAGGACA	873
OY	781	CAGTTTCACTTCGACCGAGACCCCAAGTGCCTTATTTTCCATTCACCCGCTACGAGCAG	840
Db	874	CAGTTTCACTTCGACCGAGACCCCAAGTGCCTTATTTTCCATTCACCCGCTACGAGCAG	933
OY	841	GGTATGTTCTGGGCCCACTGAAGGCTCTTAATGTGTCACACAGGTTTGGCCAAAGC	900
Db	934	GGTATGTTCTGGGCCCACTGAAGGCTCTTAATGTGTCACACAGGTTTGGCCAAAGC	993
OY	901	CAAGGATATACCATCAATGTGCTTGGAAACAGGTTGGGATGCGGAGTCTGATCATTT	960
Db	994	CAAGGATATACCATCAATGTGCTTGGAAACAGGTTGGGAGTGGGATGCTGATCATTT	1053
OY	961	GCTGCTTTCCTGACAGTCTGCTGCTGACAGTGGCCCTGAGTTCACAGCTTGTGTCCTG	1020
Db	1054	GCTGCTTTCCTGACAGTCTGCTGCTGACAGTGGCCCTGAGTTCACAGCTTGTGTCCTG	1113
OY	1021	GTCGCTCTGATTTGATGTCCTCGCAAGGGGACCCCAAGGGTATATGTCGCGCACTCG	1080
Db	1114	GTCGCTCTGATTTGATGTCCTCGCAAGGGGACCCCAAGGGTATATGTCGCGCACTCG	1173
OY	1081	GCAAGGTTTCGCCAGCTTAAACCACTGCTCATGAGGTCTGGACGAGGCAAGCTGATCTTG	1140

Db 1174 GAAAGGTTG6CCAGCTAACCCACTGCTCATGGGTCCTGCGAGAGCAGCAACTGATCTGT 1233
Qy 1141 TCTCTGAGAGGTTGGTACAAACCTCCGGGCGCTGGTGAAGGCGTCACTGCTGCTCCAC 1200
Db 1234 TCTCTGAGAGGTTGGTACAAACCTCCGGGCGCTGGTGAAGGCGTCACTGCTGCTCCAC 1293
Qy 1201 ACCCTTCTGGAGAGACCTTGGCCCATGCTGAGTCACTGGTGGCCCTCCGGAGTGGC 1260
Db 1294 ACCCTTCTGGAGAGACCTTGGCCCATGCGGAGTCACTGGTGGCCCTCCGGAGTGGC 1353
Qy 1261 CAGGCTTCAAGTTCCTGTGCTGTGAAGCCCTTGAGCCCTTCTGGAGGTTCTTGTAGA 1320
Db 1354 CAGGCTTCAAGTTCCTGTGCTGTGAAGCCCTTGAGCCCTTCTGGAGGTTCTTGTAGA 1413
Qy 1321 TCAACTGAAACCGTGGAGAGGAGCAACATGGAGAGACATGTAGAGAGAGCAGAG 1380
Db 1414 TCAACTGAAACCGTGGAGAGGAGCAACATGGAGAGACATGTAGAGAGAGCAGAG 1473
Qy 1381 GAAAGACCTGGGAGGCGCCCTGTGCTCCCAATGCTGACATGGGCGAGTCAAGTCTCGC 1440
Db 1474 GAAAGACCTGGGAGGCGCCCTGTGCTCCCAATGCTGACATGGGCGAGTCAAGTCTCGC 1533
Qy 1441 ACAGGCGTGGTCTATGACCAAAATATGATGAATCACTGCACTTGTGGACAGCCACAC 1500
Db 1534 ACAGGCGTGGTCTATGACCAAAATATGATGAATCACTGCACTTGTGGACAGCCACAC 1593
Qy 1501 CCTGAGATACCCAGAGCATCTTGGCGATCATGTGCCGTGGAGAGCTGGGCGTTCGC 1560
Db 1594 CCTGAGATACCCAGAGCATCTTGGCGATCATGTGCCGTGGAGAGCTGGGCGTTCGC 1653
Qy 1561 GGGGCGTGGCTCACCCCTGACACCGGCGCCCTGCCACAGAGGCTGAGTGCACCTGTGC 1620
Db 1654 GGGGCGTGGCTCACCCCTGACACCGGCGCCCTGCCACAGAGGCTGAGTGCACCTGTGC 1713
Qy 1621 AGTGTGATAGTGGTGTATCTCCGGGCGACAGAGAAATGAAATCCCGAGAGTGCAC 1680
Db 1714 AGTGTGATAGTGGTGTATCTCCGGGCGACAGAGAAATGAAATCCCGAGAGTGCAC 1773
Qy 1681 CGTGAAGTTCACACTTTCATCTCATCTATATCTGCCACAGTACCTTCCGCTGTGCAC 1740
Db 1774 CGTGAAGTTCACACTTTCATCTCATCTATATCTGCCACAGTACCTTCCGCTGTGCAC 1833
Qy 1741 CTGACACTGGGCGTGGCGCGCGCTGGTGGAGGCTGTCTCAGAGAGGTTCTGAAT 1800
Db 1834 CTGACACTGGGCGTGGCGCGCGCTGGTGGAGGCTGTCTCAGAGAGGTTCTGAAT 1893
Qy 1801 GGT 1860
Db 1894 GGT 1953
Qy 1861 TGTCTTTTCACTGT 1920
Db 1954 NGCTTTTCACTGT 2013
Qy 1921 CTAGGATTCCTGATTTGT 1980
Db 2014 CTAGGATTCCTGATTTGT 2073
Qy 1981 GAGGATGACCCAGT 2040
Db 2074 GAGGATGACCCAGT 2133
Qy 2041 CCCATGGGGGATGAGGGGTGCGAGCAGCAGATCGGGCGGGCTCGGGGACAGGCTTCACC 2100
Db 2134 CCCATGGGGGATGAGGGGTGCGAGCAGCAGATCGGGCGGGCTCGGGGACAGGCTTCACC 2193
Qy 2101 GTCAACGTCGATGAGAGGGGCGCGGCGATGGGTGATGCTGACTACCTGCTGCGAT 2160
Db 2194 GTCAACGTCGATGAGAGGGGCGCGGCGATGGGTGATGCTGACTACCTGCTGCGAT 2253
Qy 2161 CGCCTGTGTCTCCATTTGCTTACCGAGATTTAACCCAGAACTGTGTGTGTGTGTGTGTGT 2220
Db 2254 CGCCTGTGTCTCCATTTGCTTACCGAGATTTAACCCAGAACTGTGTGTGTGTGTGTGTGT 2313

Qy 2221 TTTGATGTGTGACGGGGGATCCGCTGGGGGCTGCCAGGTGTCACTGAGGGTTATGCC 2280
Db 2314 TTTGATGTGTGACGGGGGATCCGCTGGGGGCTGCCAGGTGTCACTGAGGGTTATGCC 2373
Qy 2281 CACCTCACCCAGCTGATGGGCTTCCAGTGGGCGCCATTTATCTTATCTTATAGGGT 2340
Db 2374 CACCTCACCCAGCTGATGGGCTTCCAGTGGGCGCCATTTATCTTATCTTATAGGGT 2433
Qy 2341 GGTATATACCTGACATCCATCTCAGAGTCACTGGCTGTGCTCACTGCTCTCTTGTGA 2400
Db 2434 GGTATATACCTGACATCCATCTCAGAGTCACTGGCTGTGCTCACTGCTCTCTTGTGA 2493
Qy 2401 GACCCACACCCCTGTGACCCCTCCAGGGCGCCCATATCAGGGGCGCTGCTCAATC 2460
Db 2494 GACCCACACCCCTGTGACCCCTCCAGGGCGCCCATATCAGGGGCGCTGCTCAATC 2553
Qy 2461 ACTGAGACATCCAAAGTCCATCCGAGATCTGGGGGAGCTTACGGGTATGAAAGTAGA 2520
Db 2554 ACTGAGACATCCAAAGTCCATCCGAGATCTGGGGGAGCTTACGGGTATGAAAGTAGA 2613
Qy 2521 GACAGAGAGAGACCCCTCAGTTCTTAAAGTGTGTCACAAAGAGGACCCCAACAGCAAA 2580
Db 2614 GACAGAGAGAGACCCCTCAGTTCTTAAAGTGTGTCACAAAGAGGACCCCAACAGCAAA 2673
Qy 2581 CCTAGGTTAGCTGAGCGGATGACACACAGAGAAAGAGTTCGTGAAGCAGGATGGGG 2640
Db 2674 CCTAGGTTAGCTGAGCGGATGACACACAGAGAAAGAGTTCGTGAAGCAGGATGGGG 2733
Qy 2641 AAAGTCACTCGGCTATTTTGGGGAAGTCCACTCCAGGCCAGACTACTCAGAGACA 2700
Db 2734 AAAGTCACTCGGCTATTTTGGGGAAGTCCACTCCAGGCCAGACTACTCAGAGACA 2793
Qy 2701 GCTGTGTGGCCCTCACTCAGAGACAGCCCTCAGAGGAGCACAAGGGGGAGCCACTGTG 2760
Db 2794 GCTGTGTGGCCCTCACTCAGAGACAGCCCTCAGAGGAGCACAAGGGGGAGCCACTGTG 2853
Qy 2761 GCCCAGACATTTCTGAGGAGCCATTTGGGGAGCCATGCTGGGCGACAGACCTCAGAG 2820
Db 2854 GCCCAGACATTTCTGAGGAGCCATTTGGGGAGCCATGCTGGGCGACAGACCTCAGAG 2913
Qy 2821 GAGGCTGTGGGGGAGGACACTCCGGAGCAGACACTCAGAGAGAGACTGTGGAGAGCC 2880
Db 2914 GAGGCTGTGGGGGAGGACACTCCGGAGCAGACACTCAGAGAGAGACTGTGGAGAGCC 2973
Qy 2881 ATTCTGACAGACCACTCAGAGAGATGCTGTTGGGGAGGCGACAGCTGGGGCACAATACC 2940
Db 2974 ATTCTGACAGACCACTCAGAGAGATGCTGTTGGGGAGGCGACAGCTGGGGCACAATACC 3033
Qy 2941 TCAGAGAGGCTGTAGAGAGGCTACACTGGCCAGACATCTTCGAGAGGAGCCATGGAG 3000
Db 3034 TCAGAGAGGCTGTAGAGAGGCTACACTGGCCAGACATCTTCGAGAGGAGCCATGGAG 3093
Qy 3001 GGAAGCAGACTGACAGACTACGTCAAGAGAGGCTCAGGGGGCAGCGAGTATCCAA 3060
Db 3094 GGAAGCAGACTGACAGAGACTACGTCAAGAGAGGCTCAGGGGGCAGCGAGTATCCAA 3153
Qy 3061 ACTGCTGTAGCCCTGAGAGCAGACACCAAGCCCAACCTCAGCTGTCAGAGGAACT 3120
Db 3154 ACTGCTGTAGCCCTGAGAGCAGACACCAAGCCCAACCTCAGCTGTCAGAGGAACT 3213
Qy 3121 ACACCCAGATATCTCCAGTACACTGATGGGAGTCTCAGAGACTTGGAGCTAGGAGC 3180
Db 3214 ACACCCAGATATCTCCAGTACACTGATGGGAGTCTCAGAGACTTGGAGCTAGGAGC 3273
Qy 3181 GAATCTCAGGGGGCTCAGAGATCTCAGGGCCAGAGAGAGAACTACTAGAGAGGCA 3240
Db 3274 GAATCTCAGGGGGCTCAGAGATCTCAGGGCCAGAGAGAGAACTACTAGAGAGGCA 3333
Qy 3241 GCTGAGGTCAGAGCAATGGCTGATGTGATGCTGATGAGGAGTCTAGGGGCTCAGTAT 3300
Db 3334 GCTGAGGTCAGAGCAATGGCTGATGTGATGCTGATGAGGAGTCTAGGGGCTCAGTAT 3393

QY	761	CAGTTTCACTTGGACAGACCCCGAGTGTCTCTATATTTTTCATCCATCCACCGCTACAGACAG	840
Db	880	CAGTTTCACTTGGACAGACCCCGAGTGTCTCTATATTTTTCATCCATCCACCGCTACAGACAG	939
QY	841	GGTAGGTTTGGCCCCACCTGGAAGGCGTCTAATCGTGTCCACACAGGTTTGGGCCAAGGC	900
Db	940	GGTAGGTTTGGCCCCACCTGGAAGGCGTCTAATCGTGTCCACACAGGTTTGGGCCAAGGC	999
QY	901	CAAGGATATACCATCATCAATGTGCCTTTGGAACCAAGTGGGAGTCCGGATGTCACTACATTT	960
Db	1000	CAAGGATATACCATCATCAATGTGCCTTTGGAACCAAGTGGGAGTCCGGGATGTCTACTACATTT	1055
QY	961	GCTGCTTTCCTCAGACGTCTGCTGTCCAGTGCCTCCGCTCGAGTTCACAGCTTCAGCTGGTCTCG	1020
Db	1060	GCTGCTTTCCTCAGACGTCTGCTGTCCAGTGCCTCCGCTCGAGTTCACAGCTTCAGCTGGTCTCG	1119
QY	1021	GTGGCTGCGGATTTTGATGCCCCGTGCAAGGGAGCCCCAAGGGGAGATGGCCGCCACCTCCG	1088
Db	1120	GTGGCTGCGGATTTTGATGCCCCGTGCAAGGGAGCCCCAAGGGGAGATGGCCGCCACCTCCG	1179
QY	1081	GCAGGGTTTCGCCACAGCTAACCCACCTGTCTCAGTGGGTCTGTGCAGAGAGGCAAGCTGATCTGTG	1148
Db	1180	GCAGGGTTTCGCCACAGCTAACCCACCTGTCTCAGTGGGTCTGTGCAGAGAGGCAAGCTGATCTGTG	1239
QY	1141	TCTCTGAGAGGGTGGCTTACACCTCCGCGCCCTGGCTGGAAGGGCTCACTGTCTTCGCTCCAC	1200
Db	1240	TCTCTGAGAGGGTGGCTTACACCTCCGCGCCCTGGCTGGAAGGGCTCAAGTGTCTTCGCTCCAC	1299
QY	1201	ACCCCTTCGGGAGACCCCTTGCCCATGTGTGAGTACACTGGTGTCCCTGCGCGAGTCC	1260
Db	1300	ACCCCTTCGGGAGACCCCTTGCCCATGTGTGAGTACACTGGTGTCCCTGCGCGAGTCC	1359
QY	1261	CAGGCTTATAGTTTCCGTGTCTGTGGAAGCCCTTGAGCCCTTCGCGGAGTTCTGTGTGA	1320
Db	1360	CAGGCTTATAGTTTCCGTGTCTGTGGAAGCCCTTGAGCCCTTCGCGGAGTTCTGTGTGA	1419
QY	1321	TCAACTGAGACCGGTGAGAGGACAACTGAGAGAGCAATGTATGAGAGAGCGAGAG	1380
Db	1420	TCAACTGAGACCGGTGAGAGGACAACTGAGAGAGCAATGTATGAGAGAGCGAGAG	1479
QY	1381	GAAAGAACCTGGGAGACCCCTGTGTCTCCCAATCCGTGAATGGCCAGTGTCTACAGTCTGC	1440
Db	1480	GAAAGAACCTGGGAGACCCCTGTGTCTCCCAATCCGTGAATGGCCAGTGTCTACAGTCTGC	1539
QY	1441	ACAGGGCTGTCTATAGACCAAAATATGATGAATCACTCAACTTGTGGAGACGACACAC	1500
Db	1540	ACAGGGCTGTCTATAGACCAAAATATGATGAATCACTCAACTTGTGGAGACGACACAC	1599
QY	1501	CCTGAGGTACCCACGACGCACTTGGCGATCATGTGCGCTGTGAGAGACTGGGCGTTGCC	1560
Db	1600	CCTGAGGTACCCACGACGCACTTGGCGAGTCATGTGCGCTGTGAGAGACTGGGCGTTGCC	1659
QY	1561	GGGGCGTCCCAACCGTCAGACCGCGCCCTCCACAGAGGCTGAGTGTCTACCTGTAC	1620
Db	1660	GGGGCGTCCCAACCGTCAGACCGCGCCCTCCACAGAGGCTGAGTGTCTACCTGTAC	1719
QY	1621	AGTGTGAGTACGTGGGTCTCATCTCCGGGCGCACAGAGAAATGAAAAACCGGGAGCTGCAC	1680
Db	1720	AGTGTGAGTACGTGGGTCTCATCTCCGGGCGCACAGAGAAATGAAAAACCGGGAGCTGCAC	1779
QY	1681	CGTAGAGATTCCAACTTTGACTCCATCTATATCTGCCCCAGTACCTTCGCTGTGCACAG	1740
Db	1780	CGTAGAGATTCCAACTTTGACTCCATCTATATCTGCCCCAGTACCTTCGCTGTGCACAG	1839
QY	1741	CTTGCACTTGGGCGTCCGCGCGCTGGTGGAGGCTGTGCTCAGAGAGAGTCTGAAT	1800
Db	1840	CTTGCACTTGGGCGTCCGCGCGCTGGTGGAGGCTGTGCTCAGAGAGAGTCTGAAT	1899
QY	1801	GGTGCTGCTGTGTGTGCTCCCGACAGACACCAAGCAGAGCAGATGACGTTCGGGTTTT	1860
Db	1900	GGTGTGCTGTGTGTGCTCCCGACAGACACCAAGCAGAGCAGATGACGTTCGGGTTTT	1959
QY	1861	TGCTTTTTCACACTGTGTGGCTGTGTGGTGTCTGCCATGCCACAGACTATACGTGGGCATGCC	1920

Db	1960	TGCTTTTCAACTGTGTGGCTGTGGCTGCCATGGCCAGACTATACAGTGGGCATGCC	2019
Qy	1921	CTACGGATCCGATGTGTGGATTTGGGATCTCCACACGSTAAATGGAATCAGACATGTTT	1980
Db	2020	CTACGGATCCGATGTGTGGATTTGGGATGTCCACACAGGTAATGGACCTCAGCACATGT	2079
Qy	1981	GAGATGACCCCAAGTGTCTATATGTGTGCCGTGACCGCTATGTATGATGGACCTTCTTC	2040
Db	2080	GAGGATGACCCCAAGTGTCTATATGTGTGCCGTGACCGCTATGTATGATGGACCTTCTTC	2139
Qy	2041	CCCATGGGGATGAGGGTGCACAGACAGATCGCGGGCTGGGGCACAGGCTTCACC	2100
Db	2140	CCCATGGGGATGAGGGTGCACAGACAGATCGCGGGCTGGGGCACAGGCTTCACC	2199
Qy	2101	GTCACAGGGGATGGAACGGGGCCCGCATGGGGTATCTACTACTACTAGCTGCTGGCAT	2160
Db	2200	GTCACAGGGGATGGAACGGGGCCCGCATGGGGTATCTACTACTACTAGCTGCTGGCAT	2259
Qy	2161	CGCGTGGTGTCCCATGTGCTACGAGTTTAAACCAAGACGGGTGTGCTCAGCTGGC	2220
Db	2260	CGCGTGGTGTCTCCCATTTGCTTACGAGTTTAAACCAAACTGGTGTGCTCAGCTGGC	2319
Qy	2221	TTTGATGCTGCACGGGGGGATCCGCTGGGGGCTGCCAGGTATCACCCTGAGGGTTATGCC	2280
Db	2320	TTTGATGCTGCACGGGGGGATCCGCTGGGGGCTGCCAGGTATCACCCTGAGGGTTATGCC	2379
Qy	2281	CACCTCACCC 2290	
Db	2380	CACCTCACCC 2389	
RESULT 4			
AAH14416			
ID	AAH14416	standard; cDNA: 2548 BP.	
XX	AAH14416;		
XX	26-JUN-2001	(first entry)	
DT			
XX	Human cDNA sequence SEQ ID NO:11863.		
DE			
XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.		
KW	Homo sapiens.		
XX	EP1074617-A2.		
PN			
XX	07-FEB-2001.		
PD			
XX	28-JUL-2000; 2000EP-0116126.		
PF			
XX	29-JUL-1999; 99JP-0248036.		
PR	27-AUG-1999; 99JP-0300253.		
PR	11-JAN-2000; 2000JP-0118776.		
PR	02-MAY-2000; 2000JP-0183767.		
PR	09-JUN-2000; 2000JP-0241899.		
XX			
PA	(HELI-) HELIX RES INST.		
XX			
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
XX	WPI: 2001-318749/34.		
DR			
XX	Primer sets for synthesizing polynucleotides, particularly the 5602		
PT	full-length cDNAs defined in the specification, and for the detection		
PT	and/or diagnosis of the abnormality of the proteins encoded by the		
PT	full-length cDNAs -		
XX			
PS	Claim 8; SEQ ID 11863; 2537pp + CD ROM; English.		
XX			
CC	The present invention describes primer sets for synthesizing 5602		


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      |||
Db      535 CACACCCCTGCTGACC--TGCACGGGCCCACTATCAGGGGCCCTGCTCAATCACTGTA 592
QY      2466 GACCATCCAAAGTCATCGAGATCTGGCGAGCTTACGGGTCAATGAAGGAGAGACAG 2525
      |||
Db      593 GACCATCCAAAGTCATCGAGATCTGGCGAGCTTACGGGTCAATGAAGGAGAGACAG 652
QY      2526 AGAAGAACCTCCAGTTCTAAGTTGGTGCACCAAGAACGCCAACCCAGCCAAACCTAG 2585
      |||
Db      653 AGAAGAACCTCCAGTTCTAAGTTGGTGCACCAAGAACGCCAACCCAGCCAAACCTAG 712
QY      2586 GTTAGCTGAGCGGATGACACAGAGAAAGAGTTCTGGAAGCAGGCAATGGGGAAGT 2645
      |||
Db      713 GTTAGCTGAGCGGATGACACAGAGAAAGAA-GTTCTGGAAGCAGGCAATGGGGAAGT 771
QY      2646 CACCTCGGCATCATTTGGGGGAAGAGTCCATCCAGGCGACACTAATCAAGACAGCTGT 2705
      |||
Db      772 CACCTCGGCATCATTTGGGGGAAGAGTCCATCCAGGCGACACTAATCAAGACAGCTGT 831
QY      2706 GGTGGCCCTCATCTCAGAGCCAGCCCTCAGAGGAGCCACAGGGGAGCCACTGTGCCCA 2765
      |||
Db      832 GGTGGCCCTCATCTCAGAGCCAGCCCTCAGAGGAGCCACAGGGGAGCCACTGTGCCCA 883
QY      2766 GACCATTTCTGAGGCGCATTTGGGGAGCCATGCTGGGCCAGACCACTCAGAGGAGGC 2825
      |||
Db      884 -----CTGGGCCAAACCACTCAGAGGAGGC 909
QY      2826 TGTCCGGGGAGGCACTCCGGACACAGCACTCAGAGGAGAGACTGTGGGAGAGCCATTCT 2885
      |||
Db      910 TGTCCGGGGAGGCACTCCGGACACAGCACTCAGAGGAGAGACTGTGGGAGAGCCATTCT 969
QY      2886 GGACACAGACCACTCAGAGGATGCTTTGGGGAGCCAGCTGGGGCCAGACTACCTCAGTA 2945
      |||
Db      970 GGACACAGACCACTCAGAGGATGCTTTGGGGAGCCAGCTGGGGCCAGACTACCTCAGTA 1029
QY      2946 GGAGGCTGTAGAGAGAGCTACACTGGCCCAAGACATCTCGAGAGGAGCCATGAGAGGAG 3005
      |||
Db      1030 GGAGGCTGTAGAGAGAGCTACACTGGCCCAAGACATCTCGAGAGGAGCCATGAGAGGAG 1089
QY      3006 CACACTGAGACAGACTACGTCAGAGAGGCTCAGAGGGGACACGAGCTATCCAAATCTCC 3065
      |||
Db      1090 CACACTGAGACAGACTACGTCAGAGAGGCTCAGAGGGGACACGAGCTATCCAAATCTCC 1149
QY      3066 TCTAGCCTCGAGACAGACCAACCAACCCCAACTCAGCTGTGACAGGAACTACAC 3125
      |||
Db      1150 TCTAGCCTCGAGACAGACCAACCAACCCCAACTCAGCTGTGACAGGAACTACAC 1209
QY      3126 CCAGATATCTCCAGTACAGTATGGGAGTCTCAGAGACTTGGAGCTAGAGCAGCAATC 3185
      |||
Db      1210 CCAGATATCTCCAGTACAGTATGGGAGTCTCAGAGACTTGGAGCTAGAGCAGCAATC 1269
QY      3186 TCAGGGGGCTCAGAAATCTCAGG--CCCCAGAGAGAGAACTACTAGAGAGGAGCAGT 3244
      |||
Db      1270 TCAGGGGGCTCAGAAATCTCAGGCCCCCAGAGAGAGAGAACTACTAGAGAGGAGCAGT 1329
QY      3245 GAGGTCAAGACATGGCTGATTCGATGCTGATGACAGGATCTAGGGGCTCACTGATCAG 3304
      |||
Db      1330 GAGGTCAAGACATGGCTGATTCGATGCTGATGACAGGATCTAGGGGCTCACTGATCAG 1389
QY      3305 CCATATTTATGCTGTGACACCACTGCCCCCTGTGCTCCCATTTGGTGCAGATGATCCCA 3364
      |||
Db      1390 CCATATTTATGCTGTGACACCACTGCCCCCTGTGCTCCCATTTGGTGCAGATGATCCCA 1449
QY      3365 TACCTGACAGAGGCTTAGAGCTGACCCCAACCTTGGGGGAGCTGTGGAACAATCCAAAGA 3424
      |||
Db      1450 TACCTGACAGAGGCTTAGAGCTGACCCAACTTGGGGGAGCTGTGGAACAATCCAAAGA 1509
QY      3425 ATTGGGTGTGTCTCTTGTCTATCAGGTCTACTGTGTCTTATCATCATGATGATGATG 3484
      |||
Db      1510 ATTGGGTGTGTCTCTTGTCTATCAGGTCTACTGTGTCTTATCATCATGATGATGATG 1569
QY      3485 TCAACACCAATGAAATTTGGAGACCCGCTGGTCTCAGTTCAGTTCAGTTCAGGCT 3544
      |||

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Db      1570 TCAACACCAATGAAATTTCTGACACCCGCTGCTCCTCAGCTACATCCAGCTGTACGCT 1629
QY      3545 GGTGTACTACTGTGACGGCTATGTCCACACCAAGGCTCTCTAGATGTGAAGACATCG 3604
      |||
Db      1630 GGTGTACTACTGTGACGGCTATGTCCACACCAAGGCTCTCTAGATGTGAAGACATCG 1689
QY      3605 CCCACGACCAAGTTTGGGAGGATATGCCCCACCCCACTAA 3648
      |||
Db      1690 CCCACGACCAAGTTTGGGAGGATATGCCCCACCCCACTAA 1733
      |||
RESULT 6
AAH06343
ID AAH06343 standard; cDNA, 638 BP.
AC AAH06343;
XX
XX 26-JUN-2001 (first entry)
Df
XX
XX Human cDNA clone (5'-primer) SEQ ID NO:3178.
DE
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX EP1074617-A2.
PN
XX
XX 07-FEB-2001.
PD
XX
XX 28-JUL-2000; 2000EP-0116126.
PF
XX
XX 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
XX
XX (HELI-) HELIX RES INST.
PA
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
PI
XX
XX WPI; 2001-318749/34.
DR
XX
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
PT
XX
XX
PS Claim 1; SEQ ID 3178; 2537pp + CD ROM; English.
XX
XX
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX in gene therapy. The primer sets can be used in antisense therapy and
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialized methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
XX AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.

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1296 GCGCTTGGAGGAGTTCTGTGAGATCACTGAGACCTGGAGAGGACAACTGAGGA 1355
 2465 CCGACCCCACTGGCCAGTGTCTGACAGCTCCAGACAGCTGAGTGTGGTGAATTCAGGA 2524
 1356 GGACATATGAGAGAG-----ACCGAGGAGGAGAGAGC 1387
 2525 TCGGATTAAGAGAGAGATCTGCACACAGGTACTGGCCATTGGATTGGTGAACACCGCC 2584
 1388 CCGGAG 1423
 2585 TATGATGTGTATACCTAGCGCGGATACGGCCATTCCGCTGCGCGAGAGAGAGAGAG 2644
 1424 -----CAGTCTACAGTCTCG 1439
 2645 CAATGCGCTGCTGTGACAGTCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2704
 1440 CACAGGGGCTGGCTTGAACCAAAATATGATGATCACTGCACTGTGGAGACAGCACA 1499
 2705 GGTGTATTATGCTTACGATGCGCAATGCTTGTGACAGTCAATTCATGATACGGGGA 2764
 1500 CCTGAGGTACCCAGCCGATCTTGGATCATGTCCGCTGTGAGAGAGCTGGGCTTGC 1559
 2765 TCCGAGAGAGCGGTGCGGCATCCAGACATCCACAAGATGACAGAGACTAGGTTGCT 2824
 1560 CGGCGCTGCTCACTGACACCGCGCTGCGACAGAGAGCTGAGCTGCTCAGCTGTCA 1619
 2825 GAAGAGATGAAGCAACTGTCCCGAGGGCGGCACACAGAGAGAGTGTGCTGCGCCA 2884
 1620 CAGTGTCTAGTACGTGGGTCTATCTCGGGCCACAGAGAGAGAGAGAGAGAGAGAGAG 1679
 2885 CACTGCGCGCCATGTAATACAGTGTGATGCTGGGCGCGAGAGAGAGAGAGAGAGAG 2944
 1680 CCGTGTAGAGTTCACAACTTGTGATCACTTATGCTGCGCCAGTACTGCTGCTGCGCA 1739
 2945 TGAGGCTGCTGGAGATCACTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 3004
 1740 GCTTGCACACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1799
 3005 CCGTGGCGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3064
 1800 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1859
 3065 CCGCATCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3124
 1860 TTGCTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1919
 3125 CTGATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3183
 1920 CTTAGGATCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1979
 3184 --AGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3241
 1980 TGAGGATGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2039
 3242 CGAGTTCACATCCCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3301
 2040 CCGCATGAGGAGATGAGGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2099
 3302 CCGCAAGGAG 3361
 2100 CGTCAAGGTGAG 2159
 3362 TGTGATACATACCTGAG 3421
 2160 TCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2219
 3422 GCACTGTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3481
 2220 CTTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2279
 3482 ATTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3541

QY 2280 CCACTTCACCCACTGCTGATGAGGCTTGGCCAGTGGCCGATTTATCCTTACAGAGCG 2339
 Db 3542 CATGCTACACCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3601
 QY 2340 TGGCTATTAACCTGATACATCCATCTCAGAGTGCATGAGTGCCTGCTGCTGCTGCT 2399
 Db 3602 TGGCTACAAATGATACCTGATTCATGAGGAGTGCATGAGTGCATGAGGAGTGCAT 3661
 QY 2400 AGACCC 2405
 Db 3662 TGAATCC 3667

RESULT 9
 AAV87399 standard; cDNA; 424 BP.
 ID AAV87399 standard; cDNA; 424 BP.
 AC AAV87399.
 XX 27-APR-1999 (first entry)
 DT EST clone CD146.
 DE
 XX Expressed sequence tag; secreted protein; haematopoiesis regulator;
 KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
 KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
 KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
 XX Homo sapiens.
 OS
 XX WO9845435-A2.
 PN 15-OCT-1998.
 PD 10-APR-1998: 98WO-US06954.
 PF 10-APR-1997: 97US-0835913.
 PR (GEM) GENETICS INST INC.
 PA Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Spaulding V, Treacy M;
 PI WPI; 1999-070076/06.
 DR
 XX New polynucleotides encoding human secreted proteins - derived from
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries
 PS
 XX Claim 1; Page 551; 633pp; English.
 CC This sequence represents an expressed sequence tag (EST), and is a
 CC polynucleotide of the invention. The polynucleotides of the invention are
 CC all secreted EST sequences isolated from a variety of human tissue
 CC sources. The EST sequences and proteins encoded by them are predicted to
 CC have useful biological activities which would make them suitable for
 CC treating, preventing or ameliorating medical conditions in humans and
 CC animals, although no supporting data is given. Suggested activities
 CC include nutritional activity, immune stimulating or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The EST sequences are also stated to be useful for gene
 CC therapy.
 CC
 SQ Sequence 424 BP; 89 A; 140 C; 109 G; 86 T; 0 other;
 Query Match 10.9%; Score 398.4; DB 20; Length 424;
 Best Local Similarity 98.5%; Pred. No. 2.3e-96;
 Matches 402; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 2178 TGCTTACAGATTAAACCCAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2237

Dd		15	TGCGCTAGAGTTTAAACCAAGAACTGTGGTGCTGCACCTGGCTTGATGCTGCACGGGG	74
Oy		2238	GGATCCGCTGGGGGGGCTGCCAAGGTGTACACTGAGGGTTATGGCCACCTCACCACTGCT	2297
Dd		75	GGATCCGCTGGGGGGGCTGCCAAGGTGTACACTGAGGGTTATGGCCACCTCACCACTGCT	134
Oy		2238	GATGGGCTTGSCCAGTAGGGCCGATTATTCCTTAATCCTAGAAGGTGGCTATACTGACATC	2357
Dd		135	GATGGGCTTGSCCAGTAGGGCCGATTATTCCTTAATCCTAGAAGGTGGCTATACTGACATC	194
Oy		2358	CATCGACAAGTCCAAAGCTGTGCTGTGACTTCGCTCCTCTTGAGAACCAACCACTGCT	2417
Dd		195	CATCGACAAGTCCAAAGCTGTGCTGTGACTTCGCTCCTCTTGAGAACCAACCACTGCT	254
Oy		2418	GACCCTGGCAGGGCCCCCATATGCATGAGGGGCCCTGGCCCAATGCATGAGACATCCAGT	2477
Dd		255	GACCCTGGCAGGGCCCCCATATGCATGAGGGGCCCTGGCCCAATGCATGAGACATCCAGT	314
Oy		2478	CCATCGCAGATACTGGCCGACGCTTACGGGCTATGAAGGTAGAAGACAGAGAAGACCTC	2537
Dd		315	CCATCGCAGATACTGGCCGACGCTTACGGGCTATGAAGGTAGAAGACAGAGAAGACCTC	374
Oy		2538	CAGTCTCTAAGTTGGTCACCAAAGAAGGCACCCCACCAACCAACCAACCTAG	2585
Dd		375	CAGTCTCTAAGTTGGTCACCAAAGAAGGCACCCCACCAACCAACCAACCTAG	422
<hr/>				
RESULT 10				
ID	AAC76966	standard; cDNA; 2461 BP.		
XX	AAC76966;			
DT	08-FEB-2001	(first entry)		
XX				
DE	Human ORF521 polynucleotide sequence SEQ ID NO:5041.			
KW	Human; open reading frame; ORF; detection; cytosolic; hepatotropic;			
KM	vulnery; antipariatic; antiparkinsonian; noctropic; neuroprotective;			
KV	anticonvulsant; osteopathic; antiarrhythmic; immunosuppressant; cardiac;			
KW	immunostimulant; thrombolytic; coagulant; vasodilator; antidiabetic;			
KV	hypotensive; dermatological; immunosuppressive; antiinflammatory;			
KW	antiviral; antibacterial; antifungal; antihemetic; antithyroid;			
KM	antiangemic; gene therapy; cancer; proliferative disorder; hypertension;			
KV	neurodegenerative disorder; osteoarthritis; graft vs host disease;			
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;			
KV	cholesterol ester storage; systemic lupus erythematosus; infection;			
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;			
KV	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;			
KM	bone damage; cartilage damage; antiinflammatory disease; coagulation;			
KW	thrombosis; contraceptive; ss.			
XX				
S5	Homo sapiens.			
XX				
PN	MO200058473-A2.			
XX				
PD	05-OCT-2000.			
XX				
PE	31-MAR-2000; 2000WO-US08621.			
XX				
PR	31-MAR-1999; 99US-0127607.			
XX				
PR	02-APR-1999; 99US-0127636.			
XX				
PR	05-APR-1999; 99US-0127728.			
XX				
PR	30-MAR-2000; 2000US-0540763.			
XX				
PA	(CURA-) CURAGEN CORP.			
XX				
PI	Shinkets RA, Leach M;			
XX				
RR	WI; 2000-602362/57.			
XX	P-PSDB; AAB42757.			
XX				

[illegible]

[illegible]

RESULT 12

AAD36979 standard; cDNA; 2022 BP

AC AAD36979;

DT 21-AUG-2002 (first entry)

DE Human histone deacetylase cDNA.

KW Human; histone deacetylase; therapy; cancer; balt protein; cytostatic;

OS Homo sapiens.

FH	key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
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91	91	91
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94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

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/ product= "Human histone deacetylase"
FT

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PN W0200230970-A2.

PD 18-APR-2002

11-OCT-2001; 2001WO-EP11759

PR 13-OCT-2000; 2000US-239928P

PA (FARB) BAYER AG.

PI zhu z;

DR WPI; 2002-416859/44.

XX

modulating agents that can be used for treating diseases such as cancer

PS Claim 1; Fig 1; 116pp; English.

The present invention relates to novel histone deacetylase proteins and polynucleotides encoding them. Sequences of the invention are useful for identifying modulating agents that are used for preventing, ameliorating or correcting dysfunctions or diseases such as cancer. They can also be used to screen for human histone deacetylase activators and inhibitors. They are useful for generating antibodies and can be used as bait proteins in two-hybrid assay or three-hybrid assay. The present sequence is a cDNA encoding human histone deacetylase.

SQ Sequence 2022 BP; 341 A; 642 C; 665 G; 374 T; 0 other;

Query Match	9.58;	Score 346;	DB 24;	Length 2022;
-------------	-------	------------	--------	--------------

Matches 571; Conservative 0; Mismatches 375; Indels 0; Gaps 0;

QY 319 GAAGGCCCTAGCGGCTCCATGCCATCAAGAGCACTGATCCAGAGGGGCTCCTAGAT 378
 Db 76 GAGCTCTTAGCGGCTTACCGGCGCCCTTGATCGGCTTGGCGGACGCGGCTTGAACAG 1355

QY	379	CGCTGCGTGCCTTTCAAGCCCGGTTTCTGAANAAGAGAGCTGATGTGGTTGCACAGC	438
Db	136	AGGTGTGCGGGTGTGACGCCCGAGGCGCTGCGAAGAGGAGACTGGGCTGGTGACAGC	195
QY	439	CTAGAAATATATTGATCTGATGGAACAACCCAGTACATGATGAGGGAGAACTCCGTGTC	498
Db	136	CCAGGTATGTATCCCTGGTCAAGGAGAGCCAGGTCCTAGGCAAGAGAGAGCTGCAGCG	255
QY	499	CTAGAGACACCTACGACTCAAGTTATATGCACTCGGAACCTCAATACCTCGTGGCCGCTG	558
Db	256	CTGTCCGACAGTTGTGACGCCATCTACTTCCACCCGAGTACCTTTTCACTGGCGCGGCTG	315
QY	559	GCGTCAGGCTGTGCTCTCAGGCTGGTGGATCGGTCCTGCGGGGCTGAAATCCGGAATGAC	618
Db	316	GCCGAGGGGCTGGAGCTCAGCTAGCTGTTGGAACGCTGTGCTCACTGAGAGCTGTCCAAATATGG	375
QY	619	ATGECATCATTTAGGCTCTCTGGAATCAGGCCCGACAGTCTTATGATGCTATTGCG	678
Db	376	CTTGCGCCGTGGAGGCGCTCCGGGACCATGACGAGAGGGGCGGTGCACAGGGGTGTGTG	435
QY	679	ATGTTCAACACAGTGTGCTGTGGCAGCCCGCTATGCTCAACAGAAACACCGCATCCGAGG	738
Db	436	GTGTTTCAACAACGTGGCCATAGCAGCTGCACATGCCAGCAAGAAACAGGGCTACACAGG	495
QY	739	GTGCTTATCGTAGATTGGGATGTGACCAAGGTCAAGGAACACAGTTACCTTGACACAG	798
Db	496	ATTCCTGTGTGGAGTGGGATGTGACCATGAGCCAGGGGATCCAGATATCTTTGAGAGAT	555
QY	799	GACCCCAAGTGTCTTATTTTCCATTCACCGCTACAGAGCAGAGGATAGTTCTGGCCCCAC	858
Db	556	GACCCCAAGTGTCTTATTTTCCATTCACCGCTACAGAGCAGAGGATAGTTCTGGCCCCAC	615
QY	859	CTGAAGGCTTAACTGCTCCACCAAGAGTTTCGGCCAGAGCCCAAGATATATCATCAT	918
Db	616	CTGGAGAGTCAATGACAGACGAGTGGGGCGGGAGACAGGGCCCTGCGCTTCACTGTCAAC	675
QY	919	GTGCTTGAACAGAGTGGGATGCGGGATGCTACATCTATGCTGCTTCTCGACAGCTC	978
Db	676	CTGCGCTGGAACAGAGTGGGATGGAAGAAACCTGATCACTAGGCTGCTTCTGACAGCTG	735
QY	979	CTGCTGCAAGTGGCCCTCGAGTTTCAGAGCTCAGAGCGGCTGAGTGTGCTGTGAT	1038
Db	736	CTGCTGCCACAGGCTTGTGAGTTTGACCTCAGCTGAGTGTGCTGTGCTGTGCGGAGATTTAC	795
QY	1039	GCCCTGCAAGGGGAGACCCCAAGGTTGAGATGGCCGCCACACTCCGGGACAGGGTTGCCACGTA	1098
Db	796	TCAGCAATCGGGAGACCTTGAGGGGCAATGAGGCGACAGGCAAGATGCTGCCACACTC	855
QY	1099	ACCAACCTGCTCATATGGGCTGTGGCAGAGGAGCAAGCTGATCTGTCTGTGAGAGGTGCTAC	1158
Db	856	ACACAGCTGTGCAAGGTGCTGTGGCGGGCGGGGCTGTGTGCTGTGGAAGGGCGGCTAC	915
QY	1159	AACCTCGCGCGCGGCTGGAAGGGGTGATGCTTTCGCTCCACACACCTTCTGGGAGACCT	1218
Db	916	CACCTGGAGTACTGTGGCGGAGTCAAGTGTGATGACAGTACAGACGCTGCTGGGTGACCG	975
QY	1219	TGCCCATATGCTGAGAGTCACTGTGTGCCCTGCGCGGAGTGGCCAGG	1264
Db	976	GCCCCACCCCTGTCAAGGGCCAAATGGCGGCATGTGACAGAGTGCAGAG	1021

RESULT 13

ID ABQ73030 standard; cDNA; 2104 BP.

AC ABQ73030;

DT 23-SEP-2002 (first entry)

DE Human HDAC9 variant HDAC9v2 encoding cDNA sequence SEQ. ID NO:7.

KM Human; HDAC9; histone deacetylase related gene; histone deacetylase
KM cytostatic; antipsoriatic; antiatherosclerotic; antiinflammatory;
KM

[illegible]

QY	ATGCCAATCATATTAAGCCCTCCGAGACATACAGCCACAGACAGTCTTATGGATGGCTATTGCG	619
Db	CTTGCCCTGGTAGAGCCTCCCGGACACCATATGGCCAGAGGGCGGCTGCCAAGGGGTTCTGT	688
QY	ATGTTTCAACACACGTGGGCTGTGGCCAGCCCGCATGCTGCTATGCATACAGAAACACCGCATCCGAGG	679
Db	GTGTTTCAACAAACGTGGCCATATGACAGTGTACATGCTCCAAAGCAACGGGCTTACACAGG	748
QY	GTCCTTATTCGTAGATTGGATGTGCACACAGGTTCAAGGAACACAGTTACCTTGGACCG	739
Db	ATCTCTCTCTGGGACTGGGATGTGCACACATGGCCAGGGGATCCAGTATCTCTTGTAGAGAT	808
QY	GACCCAGATGCTCTTATTTCTCCATATCCACCGCATACGACGAGGATAGGTTCTGGCCCCAC	799
Db	GACCCAGCGCTCTTATCTCTCTGGCACCCGCTATATAGCATATGGGCGCTTCTGGGCTTTTC	868
QY	CTGAAGGCTCTTAAGTGGTCCACACACAGGTTTGGCCAGAGGCCAAGATATATCATCAAT	859
Db	CTGCGAAGATCAGATGCAGACGCGAGTGGGCGGGGAGACAGGGCCCTCGGCTTACATCAAC	928
QY	GTCGCTTGGAAACCGATGGGGATATCCGGGATGTGTATCATATGTGCTGTTTCTGTACAGTC	919
Db	CTGCGCTGGAAACAGGTTTGGGATGGGAAACGCTGATCATGCTGTGCTTCTGTACACCTG	988
QY	CTGCTGGCAGTCCGCTCCAGATTCACACCTCAGCTGGTTCCTGGTGGGCTGTGATTTGAT	979
Db	CTGCTCCCACTGGGCTTTGAGTTTGAACCTTGAGCTGTGTGCTGTGGCAGGATTTGAC	1048
QY	GCCCTGCAGAGGAGGCCCAAGGATGAGATGGCCGCCACTCCGGCAGGGTTTCGCCACCTA	1039
Db	TCAACCATTCGGGAGCCCTTGAGGGGCAATGCAGAGGCCACGCGCAAGATGCTTCGCCACCTC	1108
QY	ACCACACTGCTCATGGGCTGTGGCAGAGGCAAGCTATCTGTCTGTGGAGGGTGGCTAC	1099
Db	ACACAGCTGTGCAGAGGTGTGGCCGGCGGGCGGGCTGTGTGCCGTGTGGAGGGGGGCTAC	1168
QY	AACCTCGCGCCCTGGGCTGAAGGGGTGAGTGTCTCGCTCCACACACCTTCTGGGAGACCT	1159
Db	CACCTGGAGTCACTGGCGGAGTCAGTGTGCATATACATACATAGACGCTGTGGTATGACCG	1228
QY	TGCCCAATGCTGGAGTCACTGTGTGCCCTGTGCCGAGTGCACAGG	1219
Db	GCCCCACCCCTGTCCAGGGCCCAATGGCGCATGTGTCCAGAGGTGGCAGG	1288

RESULT 15

AA541280

ID AA541280 standard; cdna; 1005 BP.

AA541280;

AA541280;

17-DEC-2001 (first entry)

cdna encoding novel human enzyme polypeptide #496.

Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytosolic; anti arthritic; nephrotropic; anticoagulant; ss.

Homo sapiens.

MO200155301-A2.

02-AUG-2001.

17-JAN-2001; 2001MO-US01239.

31-JAN-2000; 2000US-0179065.

04-FEB-2000; 2000US-0180628.

XX Claim 4: SEQ ID No 506; 1180bp; English.
 PS The present invention relates to the isolation of novel human enzyme
 XX polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
 CC encoding them. The enzyme polypeptides of the invention may comprise the
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
 CC isomerases or ligases. The sequences of the invention are useful in the
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of
 CC disorders including hyperproliferative disorders (e.g. cancer),
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
 CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
 CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
 CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
 CC blood-related disorders (e.g. haemophilia), reproductive disorders
 CC (e.g. infertility) and infectious disorders (e.g. Influenza). The
 CC polynucleotides of the invention can also be used in gene therapy.
 CC AAS40785-AAS41684 represent cDNA sequences encoding for the novel human
 CC enzyme polypeptides of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 XX

Sequence 1005 BP; 167 A; 313 C; 332 G; 183 T; 10 other;

Query Match 8.9%; Score 325.8; DB 22; Length 1005;

Best Local Similarity 60.7%; Pred. No. 9.8e-77;

Matches 522; Conservative 4; Mismatches 334; Indels 0; Gaps 0;

QY 319 GAAGGCGCTGAGCGGCTCCATCATCAAGAGCACTGATCCAGAGGCGCTCTAGAT 378
 DB 118 GAGCGCTGAGCGGCTCCATCATCAAGAGCACTGATCCAGAGGCGCTCTAGAT 177
 QY 379 CGCTGCGTCTCTTTCAGGCGCGGTTGCTGAAAGAGAGCTGATGTTGTTCAAGC 438
 DB 178 AGGTGCTGCGGTTGCTGAGCGCGGCTGAAAGAGAGCTGATGTTGTTCAAGC 237
 QY 439 CTAGATATATGATGATGATGAAACACACCATATGATGATGATGATGATGATGAT 498
 DB 238 CAGAGATATATGATGATGATGAAACACACCATATGATGATGATGATGATGATGAT 297
 QY 499 CTAGAGACACCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 558
 DB 298 CTGTCGGAGACATGAGCGCATCTCTCTCACCAGTACCTTCTCTCTCTCTCTCTCT 357
 QY 559 GCTTCAAGCT 618
 DB 358 GCGGAGGCGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 417
 QY 619 ATGGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 678
 DB 418 CTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 QY 679 ATGTTCAACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738
 DB 478 GTGTTCAACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
 QY 739 GTCTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 798
 DB 538 ATCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
 QY 799 GACCCAGTCT 858
 DB 598 GACCCAGTCT 657
 QY 859 CTGAAGGCGCTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 918
 DB 658 CTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
 QY 919 GTGCTTGAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 978
 DB 718 CTGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777

QY 979 CTGCTGCAAGTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1038
 DB 778 CTGCTTCCAGTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 837
 QY 1039 GCGCTGCAAGTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1098
 DB 838 TCAAGCTTCCAGTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 897
 QY 1099 ACCAGCTTCCAGTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1158
 DB 898 ACACAGCTTCCAGTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 957
 QY 1159 AACCTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1178
 DB 958 CACCTGAGTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 977

Search completed: June 13, 2003, 19:39:13
 Job time : 762 secs

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1692
US-09-115-746-1

Query Match 1.4%; Score 51.4; DB 4; Length 1695;
Best Local Similarity 44.0%; Pred. No. 0.00027;
Matches 217; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

2558 AGAAGCACCACCCACCAACCTAGTGTAGCTGCGGATGACCAACAGAGAAAGA 2617
|||||
1160 AGAAGCAGCTGAGGCCGCCAAGGCCCTGAGACGGAAGCAAGAGGAGCTTAAGCA 1219
2618 AGGTTCTGGAAGCAGGCGATGGGAAAGTCACTCGCATATTTGGGAAAGTCCACTC 2677
1220 CGAAGGTTGCCGAGAGCGAGAAAGCAAGAGGCGAGCTGAAGCCATGAAGTTCCGAAAGCGG 1279
2678 CAGGCCAGACTAACTAGAGACAGCTGTGTGCTCCTCACTCAGGACCGCTCAGAGG 2737
1280 AGAAGCAGAGGAGCAGCTGAGGCGACGAAAGTTGCCGAAAGCGAGAAAGCAGAGCAGCTG 1339
2738 CAGCCACAGGGGAGGACCTGTGGCCAGACCAATTTTGAGGCGAGCCATTGGGGAGCCA 2797
1340 AAGCCACAGAGGAGGTTGCCGAAAGCGAGAAAGCAGAGGCGAGCTGAAGCCAGAGGTTGCCG 1399
2798 TGCTGGGCGCAGACACCTCAGAGAGGCTGTCCGGGAGAGCCACCTCGGACAGACCACT 2857
1400 AAGCGAGAGAGCAGAAAGGCGAGCTGAAAGCCAGAAAGTTGCCGAAAGCGAGAGCAAGG 1459
2858 CAGAGAGACTGTGGAGAGGACCTTCTGACCAAGACCACTCAGAGAGTGTGTGGGG 2917
1460 CAGCTGAAGCCAGAGGTTGCCGAAAGCGAGAAAGCAGAGGCGAGCTGAAGCCAGCAAGG 1519
2918 GAGCCACGCTGGGCGAGACTTCACTCAGAGAGGCTGTGAGAGAGGCTTACCTGGCCAGA 2977
1520 TTGCCGAGAGCGAGAGCAGAGGACGACCTGAAAGCGAGAGGTTGCCGAGAGCGAGAGG 1579
2978 CCATCTCGAGAGGAGGACGATGAGGAGCCACACTGAGACAGACTAGCTCAGAGAGGCTC 3037
1580 AGAAGCAGACTGAAGCCAGAGAGGTTGCCGAAAGCGAGAAAGCAGAGGAGCTGAAGCCA 1639
3038 CAGGGGAGCAGCA 3050
1640 CGAAGGTTGCCGA 1652

RESULT 4
US-08-216-894-7
Sequence 7, Application US/08216894
Patent No. 5876734
GENERAL INFORMATION:
APPLICANT: Kitchoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1932 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1929
US-08-216-894-7

Query Match 1.4%; Score 51.4; DB 2; Length 1932;
Best Local Similarity 44.0%; Pred. No. 0.00029;
Matches 217; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

2558 AGAAGCACCACCCACCAACCTAGTGTAGCTGAGCGATGACCAAGAGAAAGA 2617
|||||
1160 AGAAGCAGCTGAGGCCGCCAAGGCCCTGAGAGCGAGAAAGCAGAGGAGCTGAAGCA 1219
2618 AGGTTCTGGAAGCAGGCGATGGGAAAGTCACTCGCATATTTGGGAAAGTCCACTC 2677
1220 CGAAGGTTGCCGAGAGCGAGAAAGCAGAGGCGAGCTGAAGCCATGAAGTTGCCGAAAGCGG 1279
2678 CAGGCCAGACTAACTAGAGACAGCTGTGTGCTCCTCACTCAGGACCGCTCAGAGG 2737
1280 AGAAGCAGAGGAGCAGCTGAGGCGACGAAAGTTGCCGAAAGCGAGAAAGCAGAGCAGCTG 1339
2738 CAGCCACAGGGGAGGACCTGTGGCCAGACCAATTTTGAGGCGAGCCATTGGGGAGCCA 2797
1340 AAGCCACAGAGGAGGTTGCCGAAAGCGAGAAAGCAGAGGAGCTGAAGCCAGAGGTTGCCG 1399
2798 TGCTGGGCGCAGACCACTCAGAGAGGCTGTCCGGGAGAGCCACTCGGACAGACCACT 2857
1400 AAGCGAGAGAGCAGAAAGGCGAGCTGAAAGCCAGAAAGTTGCCGAAAGCGAGAGCAAGG 1459
2858 CAGAGAGACTGTGGAGAGGACGATTCGAGACCAAGCCACAGAGATGCTGTGGGG 2917
1460 CAGCTGAAGCCAGAGGTTGCCGAAAGCGAGAGCAGAGCAGCTGAAGCCAGCAAGG 1519
2918 GAGCCACGCTGGGCGAGACTTCACTCAGAGAGGCTGTGAGAGAGCTTACCTGGCCAGA 2977
1520 TTGCCGAGAGCGAGAGAGCAGAGGAGCTGAAGCCAGCAAGGTTGCCGAAAGCGGAGAGAG 1579
2978 CCATCTCGAGAGGAGCAGCTGAGAGGAGGCGACACTGAGACAGCTTACGTAGAGAGGCTC 3037
1580 AGAAGCAGCTGAAGCCAGAGAGGTTGCCGAAAGCGAGAAAGCAGAGGAGCTGAAGCCA 1639
3038 CAGGGGAGCAGCA 3050
1640 CGAAGGTTGCCGA 1652

RESULT 5
US-09-115-746-7
Sequence 7, Application US/09115746
Patent No. 6228601
GENERAL INFORMATION:
APPLICANT: Kitchoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

Db 1112 CAGCTGAGCCAGCAGCTTCCCAAGCGAGAGACAGAGCAGCAGTCAAGCCAGCAGAG 1171
QY 2918 GAGCCAGCTGGCGCAGACTACTCAGAGAGAGCTGTAGAGAGCTACACTGGCCAGAG 2977
Db 1172 TTCCCGAAGCGGAGAGACAGAGAGCAGCTGAGAGAGGTGGCCGAGCGGAGAGAGC 1231
QY 2978 CCATCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3037
Db 1232 AGAAGGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1291
QY 3038 CAGGGGAGCAGCGA 3050
Db 1292 CGAAGGTGGCGA 1304

RESULT 7
US-09-115-746-9
; Sequence 9, Application US/09115746
; Patent No. 6228601
; GENERAL INFORMATION:
; APPLICANT: Kirchhoff, Louis V.
; APPLICANT: Otsu, Keiko
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; TITLE OF INVENTION: WITH TRYPAOSOMA CRUZI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,746
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,894
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1416
; US-09-115-746-9

Query Match 1.3%; Score 46.6; DB 4; Length 1419;
Best Local Similarity 43.4%; Pred. No. 0.0053;
Matches 214; Conservative 0; Mismatches 279; Indels 0; Gaps 0;

QY 2558 AGAAGGACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2617
Db 812 AGAAGGACCTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 871
QY 2618 AGGTCTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2677
Db 872 CGAAGGTGGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 931

QY 2678 CAGCCAGACTAATCTAGAGAGAGCTGTGTGTCCTCTCAGCAGCAGCAGCAGCAGCAGCAG 2737
Db 932 AGAAGCAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 991
QY 2738 CAGCCAGAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2797
Db 992 AAGCCAGAGAGGTTGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1051
QY 2798 TGCTGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2857
Db 1052 AAGCCAGAGAGCAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1111
QY 2858 CAGAGAGACTGTGGAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2917
Db 1112 CAGCTGAGAGCAGCAGAGGTTGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1171
QY 2918 GAGCCAGCCTGGGCGCAGACTACTCAGAGAGGCTGTAGAGAGGAGGAGGAGGAGGAGGAGG 2977
Db 1172 TTGCCGAGAGCGAGAGAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1231
QY 2978 CCATCTCGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3037
Db 1232 AGAAGGAGCTGAGAGCAGCAGAGGTTGCCGAGAGCAGAGAGCAGAGAGCAGCAGCAGCAG 1291
QY 3038 CAGGGGAGCAGCGA 3050
Db 1292 CGAAGGTGGCGA 1304

RESULT 8
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid

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;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
; CLONE: PTZgpt-F15
US-08-232-463-14

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Query Match      1.28; Score 45.6; DB 1; Length 7218;
Best Local Similarity 5.28; Pred. No. 0.024;
Matches 21; Conservative 213; Mismatches 172; Indels 0; Gaps 0
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OY	139	CTACGGGAGTAAAGAAAGAAGCGAAAATGAAGAGCTCGCCAGCATGTGAAGAAGC	198
Dd	1335	CRR	1376
OY	199	CTAATCGGGACTGCAGGATGGATGTGAACCTTGAGGCTGGAAGCACTGGCTGGCACT	258
Dd	1375	RR	1311
OY	259	GCGTTGGTGTGGATGAGCACTTAATGAATTCCATTCCTCTGGGATGACAGCTCCCG	318
Dd	1315	RRR	1250
OY	319	GAAAGCCCTGAGCGGCTCCATGCCATCAAGGACACTGATCCAGGAGGCGCTCTAGAT	378
Dd	1255	RRR	1196
OY	379	CGCTGCGTGTCTTTCAGGCCCGGTTTTCTGAAAGGAAGAGCTATGTGGTTCACAGC	438
Dd	1195	RRR	1130
OY	439	CTAGAATTTATTTGATCTGATGAAAAACAACCATGATGAATGAGGAGAACTCCGTCTC	498
Dd	1135	RRR	1076
OY	499	CTAACGACACCTACGACTCAGTTATCTGATCCGGACTATACT	544
Dd	1075	RRRRRRRRATCGAAGCTCCCTGCAGCTCAGGCCAACCTCGGAAT	1030

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RESULT 9
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294528
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007_00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

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	Query Match	1.2%:	Score 43.8:	DB 4:	Length 4411529:
	Best Local Similarity	45.1%:	Pred. No. 2.2:		
	Matches 162:	Conservative	0:	Mismatches 197:	Indels 0:
QY	2693	CAGAGACAGCGTGTGGCCCTCACTCAGSACCAACCCCTCAGAGCAGCCACAGGGGAG	2752		
Db	3942814	CAGAGCGCGCAGTGTGTGCGCGCGCGCGACGATCGTGTGCGCGCGCGCGCAAGGG	3942873		
QY	2753	CCAACTTGTGCCCAACCAATTCTCAGGAGAGCCATTGGGGGAGCCATGCTGGGCCAGACCA	2812		
Db	3942874	CGGCACACGGCGCGGACGCGCGAGATCGCGCGGGCGCGCGCGCGCACAGGGCCCAA	3942933		

Accession	Sequence	Position
OY	2813 CCTCAGAGGAGGACCTGTGCGGGAGACCCACTCCGGAGCCAGAACACCTCCAGAGGAGACTGG	2872
Db	39422934 CACCAGTCCCGCGCCCAACGCGGGGCAAGAGAGTCCAGGCGCGACCGGTGGTCCGGGG	39422933
OY	2873 GAGGAGGCATTCTGGACCCAGACCACTCAGAGATGCTGTTGGGGGAGCCACGCTGGGCC	2932
Db	39422994 GCGGCGCGGGCGTGCGGCGCCCGGTGGCGCGGCTACAGCGCACCGCTGGCAACGGGGGCA	3943053
OY	2933 AGACTACCTCAGAGGAGGCTGTAGGAGAGCTACACTGGCCAGAACCATCTTCGGAGCGAG	2992
Db	3943054 AGGCGTGTCCGGCCGCGCACCGCGCGCGCGGCGGCACTCTCACACTCAACAGCGCGCGAG	3943113
OY	2993 CCATGGAGGGAGCCACACTGGACCAAGTACCTACAGAGGAGGCTCCAGAGGGGACACCGAG	3051
Db	3943114 CGGCGGGCGCGCGCCGACACCGGAGCGAGAGGGGCGAGGGCGCGCCCGCGGCGCACCGGAG	3943172

```

RESULT 10
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

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[illegible]

```
RESULT 11
US-08-342-930-1
; Sequence 1, Application US/08342930
; Patent No. 5821084
; GENERAL INFORMATION:
; APPLICANT: OLMSTED, ELIZABETH A.
; APPLICANT: MAURO, LAURA J.
; APPLICANT: DAVIS, ALAN R.
; APPLICANT: DIXON, JACK E.
; TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; City: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,930
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-20975.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 205..5337
; US-08-342-930-1

Query Match
Best Local Similarity 1.1%; Score 40.4; DB 1; Length 5455;
Matches 101; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 3320 TGACACACTGCGCTGGTGTCCCATTTGGTGGCAGTAGTCCCATCTGACAGCAGGCC 3379
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2230 TGGGCCACAGTCTCGGGGCGCGAGCCGCTACCAAGTACCTATACAGGAGATGACC 2289
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3380 TAGACTGACCCCACTTGTGGGAGCTGTGGAAATCCAGAGAAATTGGGTGTCTCT 3439
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2290 CGGACAGCCACCGCATCATGAGGGGCCCAAGAGATGCGACGAGCTTTGGGTTGACT 2349
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3440 CTTGCAATCAGAGCTGTGTGTCGTTATCATCATGCGCAATGCTCCACACACAGTGA 3499
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2350 CCGTGGACCTAAGTACAGTGGAGATCATCTCTCTGGGCTGGGCCCTTACACTGCAGCA 2409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3500 ATTCTGACACCGCGTGTGCTCT 3521
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2410 GCCAAGCTTCTGCTGAGACT 2431
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RESULT 12
US-08-983-045-1/c
; Sequence 1, Application US/08983045
; Patent No. 6093535
; GENERAL INFORMATION:
```

```
APPLICANT: MORI, Chisato
APPLICANT: TAKAHARA, Rie
APPLICANT: OSAME, Juichiro
APPLICANT: GOMI, Yasuyuki
APPLICANT: FUKE, Isao
; TITLE OF INVENTION: METHOD FOR IDENTIFYING THE ATTENUATED VARICELLA VIRUS OKA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; City: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,045
; FILING DATE: 15-JAN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP97/01646
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-158795
; FILING DATE: 15-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 216-393P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: varicella-zoster virus
; STRAIN: attenuated varicella virus Oka strain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..486
; US-08-983-045-1

Query Match
Best Local Similarity 1.1%; Score 40.2; DB 3; Length 487;
Matches 129; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 2737 GCACCCACAGGGGAGCCATCTGTGGCCACCATTTGTGAGCAGCATTGGGGAGCC 2796
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 350 GCGGCCGAGTGGGGGCGACGCGGAGATTCGGGAAGCGGCCGAGGTGGGCGCG 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2797 ATGCTGGGCCAGACCACTCAGAGAGAGCTGTGGGGAGAGCCATCCCGACAGACACC 2856
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 290 ACGGCGGGATCGGATTTGCGGAGCGGCCAGAGTGGCGCGACGCGGGATCGGATTT 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2857 TCAGAGAGATCTGTGGAGAGACCATTTGTGACACAGACCATCTCAGAGAGTCTGTTGG 2916
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 230 CGGATAGGCGCCAGATGTGGGCGCGAGCGGGATGCGGCTTTCCGGGAAGCGGCCAGATG 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2917 GGAGCCAGCTGGGCCAGACTAATCTCAGAGAGGCTGTAGAGAGCTTACACTGCCCCAG 2976
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 170 GCGCGAGAGCGGGATCGGCTTTCGGGAAGCGGCCGAGTGGGCGCGACGCGGGATCG 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2977 ACATCTCGGAGGAGCGATGAGAGGAGCCACACTGG 3013
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Db 110 GGCCTTCGGGAAAGCGCCGAGGTGGGCGGACGCGCG 74

RESULT 13

US-08-983-045-3/c

; Sequence 3, Application US/08983045
; Patent No. 6093535

GENERAL INFORMATION:

APPLICANT: MORI, Chisato

APPLICANT: TAKAHARA, Rie

APPLICANT: OSAME, Junichiro

APPLICANT: GOMI, Yasuyuki

APPLICANT: FUKE, Isao

TITLE OF INVENTION: METHOD FOR IDENTIFYING THE ATTENUATED VARICELLA VIRUS OKA STR

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STREET: 8110 Gatehouse Road, Suite 500 East

CITY: Falls Church

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983,045

FILING DATE: 15-JAN-1998

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP97/01646

FILING DATE: 15-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-158795

FILING DATE: 15-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: SVENSSON, Leonard R.

REGISTRATION NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 216-393P(PCT)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1683 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: varicella-zoster virus

STRAIN: attenuated varicella virus Oka strain

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1683

US-08-983-045-3

Query Match

Best Local Similarity 1.1%; Score 40.2; DB 3; Length 1683;

Matches 129; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Db 2737 GCAGCCACAGGGGAGGACCTCTGCGCCAGACCATTTCTGAGGACCATTTGGGGAGCC 2796

Db 401 GCGGCGGAGGTGGGCGGACGCGGATTCGGGGAAGCGCGGAGGTGGGCGG 342

Db 2797 ATGCTGGGCGGACACCATCTCAGAGAGGCTGTGCGGGGACCATCTCGGACGACAC 2856

Db 341 ACGGGGAGATCGGATTTTCGGGAACGCGCGGAGGTGGGCGGACGCGGATTCG 282

Db 2857 TCAGAGGAGACTGTGGAGGACCATTTCTGACACGACCATCTCAGAGGATGCTGTGGG 2916

Db 281 CGGATAGCGCGCCAGAGTGGGCGGACGCGGAGATCGGCTTTTCGGAAGCGCGGAGGTG 222

Db 2917 GAGCCACGCTGGGCGGACGATACCTCAGAGAGGCTTAGAGGAGCTACACTGCGCCAG 2976

Db 221 GCGCGGCGGCGGAGTTCGGCTTTCGGGAAGCGCGGAGGTGGGCGGAGGTG 162

Db 2977 ACCATCTGGAGGCGGACGATGAGGAGCCACCATCTG 3013

Db 161 GCCTTCGGGAAGCGCGCGGAGGTGGGCGGAGGTG 125

RESULT 14

US-09-446-504-79

; Sequence 79, Application US/09446504

; Patent No. 6218150

GENERAL INFORMATION:

APPLICANT: UEMORI, Takashi

APPLICANT: SATO, Yoshimi

APPLICANT: FUJITA, Tomoko

APPLICANT: MIYAKE, Kazuo

APPLICANT: MUKAI, Hiroyuki

APPLICANT: ASADA, Kiyozo

APPLICANT: KATO, Ikunoshin

TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS

FILE REFERENCE: 1422-408PCT

CURRENT APPLICATION NUMBER: US/09/446,504

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: PCT/JP98/02845

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: JP 9-187496

PRIOR FILING DATE: 1997-06-26

PRIOR APPLICATION NUMBER: JP 9-320692

PRIOR FILING DATE: 1997-11-27

NUMBER OF SEQ ID NOS: 92

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 79

LENGTH: 1005

TYPE: DNA

ORGANISM: Pyrococcus furiosus

US-09-446-504-79

Query Match

Best Local Similarity 1.1%; Score 39.2; DB 4; Length 1005;

Matches 68; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Db 2131 GGTGATGCTGACCTACCTAGCTGCGCATCGCTGCTGCCATTTGCTACGAGTTT 2190

Db 658 GGGGATGGGATATACATATATGTTGGAGCAATTTGCTTCCATAGTTGAAGAGTT 717

Db 2191 AACCCAGACTGGTCTGCTCAGCTGCTGCTTGTATCTGCACGGGGGATCCGCT 2246

Db 718 AACCCAAAGTCAATCGAATTTCCGCGGCTTGTATGATTTAAAGGGAGTCT 773

RESULT 15

US-09-712-266-79

; Sequence 79, Application US/09712266

; Patent No. 6333158

GENERAL INFORMATION:

APPLICANT: UEMORI, Takashi

APPLICANT: SATO, Yoshimi

APPLICANT: FUJITA, Tomoko

APPLICANT: MIYAKE, Kazuo

APPLICANT: MUKAI, Hiroyuki

APPLICANT: ASADA, Kiyozo

APPLICANT: KATO, Ikunoshin

TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS

FILE REFERENCE: 1422-408PCT

CURRENT APPLICATION NUMBER: US/09/712,266

CURRENT FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: US 09/446,504

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: PCT/JP98/02845

; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: JP 9-187496
 ; PRIOR FILING DATE: 1997-06-26
 ; PRIOR APPLICATION NUMBER: JP 9-320692
 ; PRIOR FILING DATE: 1997-11-27
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 79
 ; LENGTH: 1005
 ; TYPE: DNA
 ; ORGANISM: Pyrococcus furiosus
 US-09-712-266-79

Query Match 1.18; Score 39.2; DB 4; Length 1005;
 Best Local Similarity 58.6%; Pred. No. 0.5;
 Matches 68; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 2131 GGTGATGCTGACACTAGCTAGCTGGCATCCCTGTGCTTCCCATGCTTACGAGTTT 2190
 DB 658 GGGATGGGATGATATATATGTTGGAGAAATGTGCTTCCCATATGTTGAAGAAATT 717
 QY 2191 AACCCAGAACTGGTGGCTGCTCAGCTGGCTTGTATGCTGACAGGGGGGATCGCT 2246
 DB 718 AAGCCAAAGTCTATCTATTTCGCGGGCTTGATGATTAAAGGGGATGGCTCT 773

Search completed: June 13, 2003, 16:41:18
 Job time : 213 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 16:35:13 ; Search time 484 Seconds
(without alignments)
10914.309 Million cell updates/sec

Title: US-09-800-187-5

Perfect score: 3648
Sequence: 1 atgacctcaacgcgcagga.....atagcccccacacactaa 3648

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3614.4	99.1	4099	10 US-09-817-913-12	Sequence 12, Appl
2	3614.4	99.1	4099	10 US-09-817-538-12	Sequence 12, Appl
3	346	9.5	2022	10 US-09-976-280A-1	Sequence 1, Appl
4	226.6	6.2	418	10 US-09-983-965-5409	Sequence 5409, Ap
5	210.6	5.8	3131	10 US-09-817-913-14	Sequence 14, Appl
6	210.6	5.8	3131	10 US-09-817-538-14	Sequence 14, Appl
7	194	5.3	8459	9 US-09-563-728A-31	Sequence 31, Appl
8	192.4	5.3	8459	10 US-09-817-913-8	Sequence 8, Appl
9	192.4	5.3	8459	10 US-09-817-538-8	Sequence 8, Appl
10	173.6	4.8	2233	9 US-09-563-728A-33	Sequence 33, Appl
11	173.6	4.8	2233	10 US-09-817-913-10	Sequence 10, Appl
12	173.6	4.8	2233	10 US-09-817-538-10	Sequence 10, Appl
13	153.2	4.3	3054	9 US-10-173-539-5	Sequence 5, Appl
14	153.2	4.3	3186	9 US-10-072-094-97	Sequence 97, Appl
15	155.2	4.3	3186	9 US-10-173-539-1	Sequence 91, Appl
16	155.2	4.3	3650	9 US-10-072-094-94	Sequence 94, Appl
17	155.2	4.3	4467	9 US-10-072-094-88	Sequence 88, Appl
18	155.2	4.3	7699	9 US-10-173-539-14	Sequence 14, Appl
19	143.6	3.9	452	9 US-09-796-692-4129	Sequence 4129, Ap

20	143.6	3.9	452	9 US-10-040-862-4129	Sequence 4129, Ap
21	140.4	3.8	1452	10 US-09-822-830A-585	Sequence 585, App
22	139.4	3.8	343	10 US-09-783-590-10530	Sequence 10530, A
23	137.2	3.8	313	10 US-09-833-381-1303	Sequence 1303, Ap
24	133.2	3.7	451	9 US-09-796-692-3075	Sequence 3075, Ap
25	133.2	3.7	451	9 US-10-040-862-3075	Sequence 3075, Ap
26	127	3.5	141	10 US-09-783-590-3772	Sequence 3772, Ap
27	121.8	3.3	311	10 US-09-783-590-9596	Sequence 9596, Ap
28	121.8	3.3	559	9 US-09-918-995-28035	Sequence 28035, A
29	110.4	3.0	492	9 US-09-918-995-9706	Sequence 9706, Ap
30	106.2	2.9	3209	9 US-10-072-094-106	Sequence 106, App
31	105.8	2.9	489	9 US-10-072-094-12	Sequence 12, Appl
32	105.8	2.9	2790	9 US-10-072-094-98	Sequence 98, Appl
33	105.8	2.9	3367	9 US-10-173-539-7	Sequence 7, Appl
34	105.8	2.9	3499	9 US-10-173-539-3	Sequence 3, Appl
35	105.8	2.9	3550	9 US-10-173-539-13	Sequence 13, Appl
36	105.8	2.9	7303	9 US-10-173-539-15	Sequence 15, Appl
37	83	2.3	295	10 US-09-284-093B-1185	Sequence 1185, Ap
38	75	2.1	402	9 US-09-918-995-36187	Sequence 36187, A
39	67.8	1.9	299	10 US-09-284-093B-2333	Sequence 2333, Ap
40	59.2	1.6	340	9 US-10-072-094-17	Sequence 17, Appl
41	59.2	1.6	525	9 US-10-072-094-19	Sequence 19, Appl
42	59	1.6	122186	9 US-09-563-728A-36	Sequence 36, Appl
43	56.2	1.5	6072	9 US-09-764-881-8523	Sequence 8523, Ap
44	54.6	1.5	529	9 US-10-072-094-14	Sequence 14, Appl
45	54.6	1.5	1035	10 US-09-815-242-4004	Sequence 4004, Ap

ALIGNMENTS

RESULT 1
US-09-817-913-12
Sequence 12, Application US/09817913
Patent No. US20020061860A1
GENERAL INFORMATION:
APPLICANT: Bi, Zuomei
APPLICANT: Bonfills, Claire
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.115
CURRENT APPLICATION NUMBER: US/09/817, 913
PRIOR FILING DATE: 2001-03-26
PRIORITY APPLICATION NUMBER: US 60/192,157
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 4099
TYPE: DNA
ORGANISM: Human
US-09-817-913-12

Query Match 99.1%; Score 3614.4; DB 10; Length 4099;
Best Local Similarity 99.4%; Pred. NO. 0;
Matches 3627; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY	1	ATGACCTCAACCGCCGAGATTCCACCAACACGAGCGCAAGAGTACGACAAACCC	60
DB	94	ATGACCTCAACCGCCGAGATTCCACCAACACGAGCGCAAGAGTACGACAAACCC	153
QY	61	CAGCGCCCGCCCTCAGGACTCAGTGTCTCGAAGCGCAATATTAAAGGAGCGCTT	120
DB	154	CAGCGCCCGCCCTCAGGACTCAGTGTCTCGAAGCGCAATATTAAAGGAGCGCTT	213
QY	121	CCCCGCTTATCCCAATCTAGCGAGGTAAAGAAAGCAAAATGAGAGCTCGGC	180
DB	214	CCCCGCTTATCCCAATCTAGCGAGGTAAAGAAAGCAAAATGAGAGCTCGGC	273
QY	181	CAAGCAATGGAAGAGACCTTATGTGGAGCTGCAAGGATGATCTGACCTTGAGGCT	240
DB	274	CAAGCAATGGAAGAGACCTTATGTGGAGCTGCAAGGATGATCTGACCTTGAGGCT	333

QY 241 GAACACTG6GCTGG6ACTG6GCTTGGTGGTGGATGAGCACTTAAATGAATTCATTCCTC 300
 Db 334 GAACACTG6GCTGG6ACTG6GCTTGGTGGTGGATGAGCACTTAAATGAATTCATTCCTC 393
 QY 301 TGGGATGACACTTCCGGGAAGGCCCTGAGGGCTCCATGCCATCAGAGCACTGATC 360
 Db 394 TGGGATGACACTTCCGGGAAGGCCCTGAGGGCTCCATGCCATCAGAGCACTGATC 453
 QY 361 CAGGAGGAGCCCTAGATCGCTGGCTGTCCTTCAGGCGCCGGTTGGCAAAAGGAAG 420
 Db 454 CAGGAGGAGCCCTAGATCGCTGGCTGTCCTTCAGGCGCCGGTTGGCAAAAGGAAG 513
 QY 421 CTGATGTGGTTCACAGCCTAGAAATATATGATCATGATGAAACCAACCAGTACAT 480
 Db 514 CTGATGTGGTTCACAGCCTAGAAATATATGATCATGATGAAACCAACCAGTACAT 573
 QY 481 GAGGGAACACTCCGTGTCTAGACAGACACTGACATGATTTATCTGATCCGAATCA 540
 Db 574 GAGGGAACACTCCGTGTCTAGACAGACACTGACATGATTTATCTGATCCGAATCA 633
 QY 541 TACTCCGTGCTGCTGAGGCTCAGGCTGTCCTCCAGGCTGAGGCTGAGGCTGCTG 600
 Db 634 TACTCCGTGCTGCTGAGGCTCAGGCTGTCCTCCAGGCTGAGGCTGAGGCTGCTG 693
 QY 601 GCTGAGATCCGGAATGAGCATGAGCATGAGGCTCCTGGACATCAGCCAGACAGT 660
 Db 694 GCTGAGATCCGGAATGAGCATGAGCATGAGGCTCCTGGACATCAGCCAGACAGT 753
 QY 661 CTATGATGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 Db 754 CTATGATGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 813
 QY 721 AAACACGGCATCCGAGAGGCTCTATGATGATGATGATGATGATGATGATGATGAT 780
 Db 814 AAACACGGCATCCGAGAGGCTCTATGATGATGATGATGATGATGATGATGATGAT 873
 QY 781 CAGTTCACTTGCAGACAGGAGCCAGTGTCTTATCTCATTCACACCGCTAGACAG 840
 Db 874 CAGTTCACTTGCAGACAGGAGCCAGTGTCTTATCTCATTCACACCGCTAGACAG 933
 QY 841 GGTAGTTCTGAGCCCACTGAGAGGCTCTAATGCTGCACACAGTTTGGCCAAAGC 900
 Db 934 GGTAGTTCTGAGCCCACTGAGAGGCTCTAATGCTGCACACAGTTTGGCCAAAGC 993
 QY 901 CAAGGATATACCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 Db 994 CAAGGATATACCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1053
 QY 961 GCTGCTTCTGACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 Db 1054 GCTGCTTCTGACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113
 QY 1021 GTGGCTGCTGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 Db 1114 GTGGCTGCTGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173
 QY 1081 GCAAGGATCCGCGACGCTACACCACTGCTCATGAGGCTGCAAGAGGCAAGCTGATCTG 1140
 Db 1174 GCAAGGATCCGCGACGCTACACCACTGCTCATGAGGCTGCAAGAGGCAAGCTGATCTG 1233
 QY 1141 TCTCTGAGGAGTGGCTACCACTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 Db 1234 TCTCTGAGGAGTGGCTACCACTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1293
 QY 1201 ACCCTTGGAGAGACCTTGGCCCATGCTGAGATCAGCTGAGTGCCTGCGGAGTGC 1260
 Db 1294 ACCCTTGGAGAGACCTTGGCCCATGCTGAGATCAGCTGAGTGCCTGCGGAGTGC 1353
 QY 1261 CAGGCTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 Db 1354 CAGGCTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1413
 QY 1321 TCAACTGAGACCGTGGAGGAGCAACATGAGAGAGCAATGTAGAGAGAGAGAG 1380

Db 1414 TCAACTGAGACCGTGGAGGAGCAACATGAGAGAGCAACATGTAGAGAGAGAGAGAG 1473
 QY 1381 GAGGAGCCCTGGAGAGCCCTGCTGCTCCCAATCTGACATGCGAGTGTCTACAGTCCG 1440
 Db 1474 GAGGAGCCCTGGAGAGCCCTGCTGCTCCCAATCTGACATGCGAGTGTCTACAGTCCG 1533
 QY 1441 ACAGGAGTGTGTATGACCAATAATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1534 ACAGGAGTGTGTATGACCAATAATGATGATGATGATGATGATGATGATGATGATGAT 1593
 QY 1501 CTTGAGATACCCAGCAGCATCTTGGGATCATGATGCTGCTGAGAGAGTGGGCTTGGC 1560
 Db 1594 CTTGAGATACCCAGCAGCATCTTGGGATCATGATGCTGCTGAGAGAGTGGGCTTGGC 1653
 QY 1561 GGGCGCTGCTACCCCTGACACCGCGCCCTGCCACAGAGGCTGAGTGTCTACCTGTAC 1620
 Db 1654 GGGCGCTGCTACCCCTGACACCGCGCCCTGCCACAGAGGCTGAGTGTCTACCTGTAC 1713
 QY 1621 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Db 1714 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1773
 QY 1681 GGTGAGATTTCCAACTTGTACTCATCTATATCTGCCCCAGTACCTTCCCTGTGCACAG 1740
 Db 1774 GGTGAGATTTCCAACTTGTACTCATCTATATCTGCCCCAGTACCTTCCCTGTGCACAG 1833
 QY 1741 CTGGCACTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
 Db 1834 CTGGCACTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1893
 QY 1801 GGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 Db 1894 GGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1953
 QY 1861 TGTCTTTTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
 Db 1954 TGTCTTTTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2013
 QY 1921 CTACGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 Db 2014 CTACGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2073
 QY 1981 GAGGATGACCCAGTGTCTATATGATGATGATGATGATGATGATGATGATGATGAT 2040
 Db 2074 GAGGATGACCCAGTGTCTATATGATGATGATGATGATGATGATGATGATGATGAT 2133
 QY 2041 CCCATGGGAGTGAAGGATGCGCAGACAGATCGGCGGGCTGCGGGGACAGAGCTTCCAC 2100
 Db 2134 CCCATGGGAGTGAAGGATGCGCAGACAGATCGGCGGGCTGCGGGGACAGAGCTTCCAC 2193
 QY 2101 GTCAACGATGAGTGAAGGAGCCCGCATGAGTGGTGAATGCTACTACTGCTGCGAT 2160
 Db 2194 GTCAACGATGAGTGAAGGAGCCCGCATGAGTGGTGAATGCTACTACTGCTGCGAT 2253
 QY 2161 CGCTGCTGCTTCCCATTTGCTACGATTTAAACCAAGAACTGCTGCTGCTGCTGCTGCT 2220
 Db 2254 CGCTGCTGCTTCCCATTTGCTACGATTTAAACCAAGAACTGCTGCTGCTGCTGCTGCT 2313
 QY 2221 TTTGATGCTGACAGGAGGAGATCCGCTGGGAGGCTGCGAGGCTGCACTGAGGATTTAGCC 2280
 Db 2314 TTTGATGCTGACAGGAGGAGATCCGCTGGGAGGCTGCGAGGCTGCACTGAGGATTTAGCC 2373
 QY 2281 CACCTCACCACTGCTGATGAGGCTTGCAGTGGCCCGCATTTATCTTATCTAGAGGCT 2340
 Db 2374 CACCTCACCACTGCTGATGAGGCTTGCAGTGGCCCGCATTTATCTTATCTAGAGGCT 2433
 QY 2341 GGTCTTAACCTGACATCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
 Db 2434 GGTCTTAACCTGACATCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2493
 QY 2401 GACCCACACCCCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460

Dd	2494	UACCCAGCACCCCTCTCTGAACCTTGGCCAGGGCCCCCAATATAGAGGGGCGCTGGCCAAATTC	2553
Qy	2461	ACTGAGACCATTCGAAGTCCATTCGACGATACAGGCGCACCTTACGGGTGATGAGGTAGAA	2520
Dd	2554	ACTGAGACCATTCGAAGTCCATTCGACGATACAGGCGCACCTTACGGGTGATGAGGTAGAA	2613
Qy	2521	GACAGAGAAAGACCCCTCCAGTTCTTAAGTTGGTCACCAAGAAAGGCACCCCAACGAGCCAA	2580
Dd	2614	GACAGAGAAAGACCCCTCCAGTTCTTAAGTTGGTCACCAAGAAAGGCACCCCAACGAGCCAA	2673
Qy	2581	CCTAGGTTAGCTGAGCGGATGACCAACAGAAAAAAGAGTTCTTGGAAGCGCATGGGG	2640
Dd	2674	CCTAGGTTAGCTGAGCGGATGACCAACAGAAAAAAGAGTTCTTGGAAGCGCATGGGG	2733
Qy	2641	AAAGCACCTCGGCAATCTTTGGGGAAGATCCACTCCAGGCGAGACTAATCCAGAGCA	2700
Dd	2734	AAAGCACCTCGGCAATCTTTGGGGAAGATCCACTCCAGGCGAGACTAATCCAGAGCA	2793
Qy	2701	GCTGTGGTGGCCCTACTCAGAGACCCCTCAGAGGACGACAGAGGGGGAGCCACTCTG	2760
Dd	2794	GCTGTGGTGGCCCTACTCAGAGACCCCTCAGAGGACGACAGAGGGGGAGCCACTCTG	2853
Qy	2761	GCCCAAGACATTTCTGAGGCGACCATTTGGGGAGCGCATGCTGGGCGACACCACTCAGAG	2820
Dd	2854	GCCCAAGACATTTCTGAGGCGACCATTTGGGGAGCGCATGCTGGGCGACACCACTCAGAG	2913
Qy	2821	GAGCGTGCGGGGGAGCCACTCCGGACCAACACTCAGAGAGACTCTGTTGGAGAGCC	2880
Dd	2914	GAGCGTGCGGGGGAGCCACTCCGGACCAACACTCAGAGAGACTCTGTTGGAGAGCC	2973
Qy	2881	ATTCTGACACAGACCACTCAGAGAGATCTTTGGGGAGCGCACGTTGGCGCAACATAC	2940
Dd	2974	ATTCTGACACAGACCACTCAGAGAGATCTTTGGGGAGCGCACGTTGGCGCAACATAC	3033
Qy	2941	TCAGAGGAGGCTGTATGAGAGAGCTACACTGGCCCCAGACATCTTGGAGGCGCATGAG	3000
Dd	3034	TCAGAGGAGGCTGTATGAGAGAGCTACACTGGCCCCAGACATCTTGGAGGCGCATGAG	3093
Qy	3001	GGAGCGACACTGGAGACAGACTACGTCAGAGAGAGGCTCCAGGGGGACCGAGCTCATGCCA	3060
Dd	3094	GGAGCGACACTGGAGACAGACTACGTCAGAGAGAGGCTCCAGGGGGACCGAGCTCATGCCA	3153
Qy	3061	ACTCCTTAGCCCTCGAGACAGACACCCAGACCCCCCAACCTCAGCTGTGCAAGGAACT	3120
Dd	3154	ACTCCTTAGCCCTCGAGACAGACACCCAGACCCCCCAACCTCAGCTGTGCAAGGAACT	3213
Qy	3121	ACACCCCCAGATATCTCCCATGACACTATTTGGAGTCTCAGAGACCTTGGAGCTAGGACG	3180
Dd	3214	ACACCCCCAGATATCTCCCATGACACTATTTGGAGTCTCAGAGACCTTGGAGCTAGGACG	3273
Qy	3181	GAATCTCAGGGGGCCTCAGATCTCAGGCCCCAGAGAGGGAACCTACATAGAGGAGGCA	3240
Dd	3274	GAATCTCAGGGGGCCTCAGATCTCAGGCCCCAGAGAGGGAACCTACATAGAGGAGGCA	3333
Qy	3241	GCTGAGGTCAGAGACATGCTGATTCGATGCTGATGACAGGGAATCTAGGGGCTCAGTAT	3300
Dd	3334	GCTGAGGTCAGAGACATGCTGATTCGATGCTGATGACAGGGAATCTAGGGGCTCAGTAT	3393
Qy	3301	CAGGCCATATTTTATGCTGTACACACACTGCCCTGGTGTCCCAATTTGGTGGCATGTGC	3360
Dd	3394	CAGGCCATATTTTATGCTGTACACACACTGCCCTGGTGTCCCAATTTGGTGGCATGTGC	3453
Qy	3361	CCCATACCTGAGAGGCGTATGAGAGTACCCCAACTTGGGGGAGCTGTGGAAACAATCCAA	3420
Dd	3454	CCCATACCTGAGAGGCGTATGAGAGTACCCCAACTTGGGGGAGCTGTGGAAACAATCCAA	3513
Qy	3421	GAGAAATGGGTGTCTCTCTCTGCTATCAGGCTACGTGGTCTTACATCAATGGCCAC	3480
Dd	3514	GAGAAATGGGTGTCTCTCTCTGCTATCAGGCTACGTGGTCTTACATCAATGGCCAC	3573
Qy	3481	ATGCTCCAAACCAATGGAAATTCGAGACACCCCGTGGTCTCAGCTACATCGACTGTCA	3540
Dd	3574	ATGCTCCAAACCAATGGAAATTCGAGACACCCCGTGGTCTCAGCTACATCGACTGTCA	3633

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Oy      3541  GCGGGGTACTACTGTGCAGAGCCCTATGTCACACACAGGCTGCTAGATGTGAAGAAC 3600
Db      3694  GCTTGGGGTTACTCTCTGTCCAGGCTTATGTCACACACAGGCTCTCTAGATGTGAAGAAC 3693

Oy      3601  ATCCGCCACACAGAAAGTTTGGGGAGATATGCCCCACCCACACTAA 3648
Db      3694  ATCCGCCACACAGAAAGTTTGGGGAGATATGCCCCACCCACACTAA 3741

RESULT 2
US-09-817-538-12
; Sequence 12, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfills, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; TITLE OF INVENTION: Deacetylase Isoforms
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 4099
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-12

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Query Match	Similarity	99.1%	Score 3614.4	DB 10	Length 4099
Best Local Match	Similarity	99.4%	Pred. No. 0		
Matches 362/	Conservative	0	Mismatches	21	Indels 0
					Gaps 0
QY	1	ATGACCTCAACCGGCCAGATTCACACACAACAGGAGGGAAGATAGCAGAACCC	60		
Db	94	ATGACCTCAACCGGCCAGATTCACACACAACAGGAGGGAAGATAGCAGAACCC	153		
QY	61	CAGTCGCCCCCTCAGAGACTCCAGTGTCACTTCGAGCGGAATATTAAAGAGACCGTT	120		
Db	154	CAGTCGCCCCCTCAGAGACTCCAGTGTCACTTCGAGCGGAATATTAAAGAGACCGTT	213		
QY	121	CCCCGCTCTATCCCAATCTAGCGGAGGTAAAGAAAGGCAAAATGAAAGAACTCGC	180		
Db	214	CCCCGCTCTATCCCAATCTAGCGGAGGTAAAGAAAGGCAAAATGAAAGAACTCGC	273		
QY	181	CAAGCAATGGAAGAAAGACTTAATCGTGGAGCTGCAGGGATGATGAACTTGAAGCT	240		
Db	274	CAAGCAATGGAAGAAAGACTTAATCGTGGAGCTGCAGGGATGATGAACTTGAAGCT	333		
QY	241	GAAGCACTGGCTGGCACTGGCTTGGTTGGATGAGACGTAATGAATCCATTGCGTC	300		
Db	334	GAAGCACTGGCTGGCACTGGCTTGGTTGGATGAGACGTAATGAATCCATTGCGTC	393		
QY	301	TGGGATGACAGCTTCCCGGAAGGCCCTGAGCGGCTCCATCCATCAAGAGAGCACTGATC	360		
Db	394	TGGGATGACAGCTTCCCGGAAGGCCCTGAGCGGCTCCATCCATCAAGAGAGCACTGATC	453		
QY	361	CAGGAGGCGCTCCTAGATCGCTCGCTGCTCTTTCAGGCGCCGCTTCTCTGAAAAGAAAG	420		
Db	454	CAGGAGGCGCTCCTAGATCGCTCGCTGCTCTTTCAGGCGCCGCTTCTCTGAAAAGAAAG	513		
QY	421	CTGATGTGGTTTACAGACCTAGAAATATTGATCTGATGAAACAACCCAGTACATGAAT	480		
Db	514	CTGATGTGGTTTACAGACCTAGAAATATTGATCTGATGAAACAACCCAGTACATGAAT	573		
QY	481	GAGGAGAAATCGGTGCTAGAGAGACACTAGACATCAATTTATCTGATCGGAATCA	540		
Db	574	GAGGAGAAATCGGTGCTAGAGAGACACTAGACATCAATTTATCTGATCGGAATCA	633		

QY	541	TACTCTTGGCTGGCTGAGGCTCTGCTCAGGCTGGTGGATGGCTCTGGGG	600
Db	634	TACTCTTGGCTGGCTGAGGCTCTGCTCAGGCTGGTGGATGGCTCTGGGG	693
QY	601	GCTGAGATCCGGAATGGCATGATATAGGCTCTGAGACATCAGGCCAGCACAGT	660
Db	694	GCTGAGATCCGGAATGGCATGATATAGGCTCTGAGACATCAGGCCAGCACAGT	753
QY	661	CTTATGATGGCTATTTGATGTTCAACACAGTGGCTGGAGCCGCTATGATCAACAG	720
Db	754	CTTATGATGGCTATTTGATGTTCAACACAGTGGCTGGAGCCGCTATGATCAACAG	813
QY	721	AAACACCCGATCCGAGGGCTCTTATGCTAGATTGGATGGACCAACGCTCAAGAA	780
Db	814	AAACACCCGATCCGAGGGCTCTTATGCTAGATTGGATGGACCAACGCTCAAGAA	873
QY	781	CAGTTACCTTGGACAGGACCCAGTCCCTATTTCTCCATCCACCGCTACGACAG	840
Db	874	CAGTTACCTTGGACAGGACCCAGTCCCTATTTCTCCATCCACCGCTACGACAG	933
QY	841	GGAAGGTTCTGGCCCACTGAAGGCTCTTAAGTGTTCACACAGGTTTGGCCAAAGC	900
Db	934	GGAAGGTTCTGGCCCACTGAAGGCTCTTAAGTGTTCACACAGGTTTGGCCAAAGC	993
QY	901	CAAGGATATCCATCAATATGCTCTTGGAAACAGGTGGGATGGGATGCTGATCAATT	960
Db	994	CAAGGATATCCATCAATATGCTCTTGGAAACAGGTGGGATGGGATGCTGATCAATT	1053
QY	961	GCTGTTTCCCTGACAGTCTGCTGCAATGCCCTCGAGTTCCAGCTCAGCTGGTCTG	1020
Db	1054	GCTGTTTCCCTGACAGTCTGCTGCAATGCCCTCGAGTTCCAGCTCAGCTGGTCTG	1113
QY	1021	GTGGCTGATTTGATGCTGCTGCAAGGGAGCCCAAGGGTGGATGGCCGACCTCCG	1080
Db	1114	GTGGCTGATTTGATGCTGCTGCAAGGGAGCCCAAGGGTGGATGGCCGACCTCCG	1173
QY	1081	GCAGGGTTGCGCCACAGCTAACCCACCTGCTCATGGGTCTGGCAGGAGGCAAGCTGATCTG	1140
Db	1174	GCAGGGTTGCGCCACAGCTAACCCACCTGCTCATGGGTCTGGCAGGAGGCAAGCTGATCTG	1233
QY	1141	TCTGTGGAGGGGTGATTAACCTCCGCGCCCTGCTGAAAGGCTGATGCTTCCTCCAC	1200
Db	1234	TCTGTGGAGGGGTGATTAACCTCCGCGCCCTGCTGAAAGGCTGATGCTTCCTCCAC	1293
QY	1201	ACCCCTTGGAGAGACCTTGGCCCATGCTGGAATGACCTGGTGGCCCTGCGAGTGGC	1260
Db	1294	ACCCCTTGGAGAGACCTTGGCCCATGCTGGAATGACCTGGTGGCCCTGCGAGTGGC	1353
QY	1261	CAGGCTTCAATTTCTGTGCTGTGGAAACCTTGAAGCCCTTCTGGAGGTTCTTGTAGA	1320
Db	1354	CAGGCTTCAATTTCTGTGCTGTGGAAACCTTGAAGCCCTTCTGGAGGTTCTTGTAGA	1413
QY	1321	TCAACTGAGACCGTGGAGAGGAGACATGAGAGAGACATGTGAGAGAGAGAGAG	1380
Db	1414	TCAACTGAGACCGTGGAGAGGAGACATGAGAGAGACATGTGAGAGAGAGAGAG	1473
QY	1381	GAAAGACCTTGGAGAGCCCTGTGCTCCATCTGACATGGCCAGAGTCTCACTGCGC	1440
Db	1474	GAAAGACCTTGGAGAGCCCTGTGCTCCATCTGACATGGCCAGAGTCTCACTGCGC	1533
QY	1441	ACAGGGCTGTCTATGACCAAAATATGATGATCACTGCAACTGTGGAGACAGCCACAC	1500
Db	1534	ACAGGGCTGTCTATGACCAAAATATGATGATCACTGCAACTGTGGAGACAGCCACAC	1593
QY	1501	CCTGAGGATACCCAGCCGATCTTGGCGATCATGTGCGCTCTGGAGAGAGCTGGGCTTGGC	1560
Db	1594	CCTGAGGATACCCAGCCGATCTTGGCGATCATGTGCGCTCTGGAGAGAGCTGGGCTTGGC	1653
QY	1561	GGGGCTCTCTACACCTGACACCGGCTGCTCACAAGAGGCTGAGTCTCACTGTCAC	1620
Db	1654	GGGGCTCTCTACACCTGACACCGGCTGCTCACAAGAGGCTGAGTCTCACTGTCAC	1713
QY	1621	AGTGTGAGTACGTGGGTATCTCCGGGACACAGAGAAATGAATAACCGGGAGCTGCAC	1680
Db	1714	AGTGTGAGTACGTGGGTATCTCCGGGACACAGAGAAATGAATAACCGGGAGCTGCAC	1773
QY	1681	CGTGAAGTCCCAACTTTGATCCATCTATATCTGGCCCAAGTACCTTCCCTGTGCACAG	1740
Db	1774	CGTGAAGTCCCAACTTTGATCCATCTATATCTGGCCCAAGTACCTTCCCTGTGCACAG	1833
QY	1741	CTTGGCACTGGCCCTGCTCCGCTGGTGGAGAGCTGTGCTCAGAGAGTTCAT	1800
Db	1834	CTTGGCACTGGCCCTGCTCCGCTGGTGGAGAGCTGTGCTCAGAGAGTTCAT	1893
QY	1801	GGTGTGCTGTGGTGGTCCCGCAGACACACGACAGAGATGACAGTTCGGT	1860
Db	1894	GGTGTGCTGTGGTGGTCCCGCAGACACACGACAGAGATGACAGTTCGGT	1953
QY	1861	TGCTTTTCAACTGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGC	1920
Db	1954	TGCTTTTCAACTGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGC	2013
QY	1921	CTACGGATCCTGATTTGATTTGGATTTGTCACACAGGTAAATGAATCAAGACATGTT	1980
Db	2014	CTACGGATCCTGATTTGATTTGGATTTGTCACACAGGTAAATGAATCAAGACATGTT	2073
QY	1981	GAGGATGACCCAGTGTCTATATGTGTCCCTGACACCGTATGATATGGACCTTCTTC	2040
Db	2074	GAGGATGACCCAGTGTCTATATGTGTCCCTGACACCGTATGATATGGACCTTCTTC	2133
QY	2041	CCCATGGGGATGAGGGTGGCACACACAGATGGCCGGGGCTCCGGGGACAGGCTTCAC	2100
Db	2134	CCCATGGGGATGAGGGTGGCACACACAGATGGCCGGGGCTCCGGGGACAGGCTTCAC	2193
QY	2101	GTCAGGTGGATGAGAGGGGCCCCGATAGGGATGATGATCTACCTACCTCCCTGGCAT	2160
Db	2194	GTCAGGTGGATGAGAGGGGCCCCGATAGGGATGATGATCTACCTACCTCCCTGGCAT	2253
QY	2161	CGCTGGTGTCCATTTGCTTACGAGTTTAAACCCAGAACTGGTGTCTCAGCTGGC	2220
Db	2254	CGCTGGTGTCCATTTGCTTACGAGTTTAAACCCAGAACTGGTGTCTCAGCTGGC	2313
QY	2221	TTTGTATGCTGACAGGGGGGATCCGGGGGGGGTGGCAGATGTCACCTGAGGGTTATGGC	2280
Db	2314	TTTGTATGCTGACAGGGGGGATCCGGGGGGGGTGGCAGATGTCACCTGAGGGTTATGGC	2373
QY	2281	CACCTACCCACTGCTGATAGGGCTTGGCAGTGGCCGATTAATCTTATCTAGAGGCT	2340
Db	2374	CACCTACCCACTGCTGATAGGGCTTGGCAGTGGCCGATTAATCTTATCTAGAGGCT	2433
QY	2341	GGCTATTAACCTGACATCATCTCAGAGTCCATGAGTGGCTGCACTGCTCCTTGA	2400
Db	2434	GGCTATTAACCTGACATCATCTCAGAGTCCATGAGTGGCTGCACTGCTCCTTGA	2493
QY	2401	GACCCACACCCCTGCTGACCCCTGGACAGGGCCCACTTACAGGGGGCCCTGGCTCAATC	2460
Db	2494	GACCCACACCCCTGCTGACCCCTGGACAGGGCCCACTTACAGGGGGCCCTGGCTCAATC	2553
QY	2461	ACTGAGACCATCCAACTGATGAGGCTTGGCAGTGGCCGAGCTTACGGGTCTAGAGTAGAA	2520
Db	2554	ACTGAGACCATCCAACTGATGAGGCTTGGCAGTGGCCGAGCTTACGGGTCTAGAGTAGAA	2613
QY	2521	GACAGAGAGACCTTCACGTTCTAAGTTGGTCCACAGAGGACCCCAACAGCCAAA	2580
Db	2614	GACAGAGAGAGACCTTCACGTTCTAAGTTGGTCCACAGAGGACCCCAACAGCCAAA	2673
QY	2581	CCTAGGTTTACGTGAGGGGATGACCAACAGAGAAAAGAGTTCTGGAACAGGCAATGGGG	2640
Db	2674	CCTAGGTTTACGTGAGGGGATGACCAACAGAGAAAAGAGTTCTGGAACAGGCAATGGGG	2733
QY	2641	AAAGTACACTGGGCATCTTTGGGGAAGAGTCCACATCCAGGCCAGACTAATCAGAGACA	2700
Db	2734	AAAGTACACTGGGCATCTTTGGGGAAGAGTCCACATCCAGGCCAGACTAATCAGAGACA	2793
QY	2701	GCTGTGTGGCCCTCAGTACAGACAGCCCTCAGAGGACCCACAGGGGGAGCCACTGTG	2760

Db 2794 GCTGTGTTGGCCCTTCACTCAGGACCAAGCCCTCAGAGGACGCCACAGGGGAGCCACTCTG 2853
 Qy 2761 GCCAGACCAATTTTGTAGGACGAGCCATTGGGGAGCCATTGCTGGCCAGACCACTCAGAG 2820
 Db 2854 GCCAGACCAATTTTGTAGGACGAGCCATTGGGGAGCCATTGCTGGCCAGACCACTCAGAG 2913
 Qy 2821 GAGGCTGTGGGGGAGCCACTCCGAGACAGACCACTCAGAGGAGAGCTGTGGGAGAGCC 2880
 Db 2914 GAGGCTGTGGGGGAGCCACTCCGAGACAGACCACTCAGAGGAGAGCTGTGGGAGAGCC 2973
 Qy 2881 ATTCTGGACCAAGACCACTCAGAGAGATGCTTTGGGGAGCCAGAGCTGGCCAGACTACC 2940
 Db 2974 ATTCTGGACCAAGACCACTCAGAGAGATGCTTTGGGGAGCCAGAGCTGGCCAGACTACC 3033
 Qy 2941 TCAGAGAGGCTGTAGAGAGACTACACTGTGGCCAGACCACTCTGGAGGACCACTGAG 3000
 Db 3034 TCAGAGAGGCTGTAGAGAGACTACACTGTGGCCAGACCACTCTGGAGGACCACTGAG 3093
 Qy 3001 GAGGCCAACAATGACCACTCAGAGAGAGCTCCAGGGGAGCCAGAGCTGATCCAA 3060
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 Qy 3061 ACCTCTTACCTCTGACAGACAGACCAAGACCCCAACCTGACCTGTGACAGGAACT 3120
 Db 3154 ACCTCTTACCTCTGACAGACAGACCAAGACCCCAACCTGACCTGTGACAGGAACT 3213
 Qy 3121 ACAACCCAGATATCTCCAGTACACTGATTTGGAGTCTCAGAGACTTGGAGCTAGGAGC 3180
 Db 3214 ACAACCCAGATATCTCCAGTACACTGATTTGGAGTCTCAGAGACTTGGAGCTAGGAGC 3273
 Qy 3181 GAATCTCAGAGGGGCTCAGAACTCAGAGCCCAAGAGAGAACTACTAGAGAGAGCA 3240
 Db 3274 GAATCTCAGAGGGGCTCAGAACTCAGAGCCCAAGAGAGAACTACTAGAGAGAGCA 3333
 Qy 3241 GCTGAGAGTAGAGCATGAGCTGATTCGATGCTGATGAGAGGATCAGAGGGGCTCAGTAT 3300
 Db 3334 GCTGAGAGTAGAGCATGAGCTGATTCGATGCTGATGAGAGGATCAGAGGGGCTCAGTAT 3393
 Qy 3301 CAGGCCAATATTTATGCTGTGACACCACTGCTGTGCTCCCACTTTGGTGGCAGTATGC 3360
 Db 3394 CAGGCCAATATTTATGCTGTGACACCACTGCTGTGCTCCCACTTTGGTGGCAGTATGC 3453
 Qy 3361 CCCATACCTCAGAGAGCCCTAGAGCTAGACCACTTGTGGGAGCTGTGGAACAATCCAA 3420
 Db 3454 CCCATACCTCAGAGAGCCCTAGAGCTAGACCACTTGTGGGAGCTGTGGAACAATCCAA 3513
 Qy 3421 GAGAAATGGGTGTGCTCTGCTGCTATCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
 Db 3514 GAGAAATGGGTGTGCTCTGCTGCTATCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3573
 Qy 3481 ATGCTCCACACCACTGAGAAATTTGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
 Db 3574 ATGCTCCACACCACTGAGAAATTTGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3633
 Qy 3541 GCTGTGTTACTACTGTGAGGCTATGCTCAGACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
 Db 3634 GCTGTGTTACTACTGTGAGGCTATGCTCAGACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3693
 Qy 3601 ATGCCCCACCAAGAACTTTGGGAGGATATGCCCAACCACTGAA 3648
 Db 3694 ATGCCCCACCAAGAACTTTGGGAGGATATGCCCAACCACTGAA 3741

RESULT 3
 US-09-976-280A-1
 ; Sequence 1, Application US/09976280A
 ; Patent No. US20020115177A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhi, Zhimin
 ; TITLE OF INVENTION: Regulation of Human Histone Deacetylase
 ; FILE REFERENCE: 004974.00590
 ; CURRENT APPLICATION NUMBER: US/09/976, 280A
 ; CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: US 60/239,928
 ; PRIOR FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 2022
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-976-280A-1

Query Match 9.5%; Score 346; DB 10; Length 2022;
 Best local similarity 60.4%; Pred No. 4.9e-95;
 Matches 571; Conservative 0; Mismatches 375; Indels 0; Gaps 0;

Qy 319 GAAGCCCTGAGCCGCTCCATCCATCAAGAGCACTATCCAGAGAGGCGCTCTAGAT 378
 Db 76 GAGGCTCTGAGCGGCTGAGCCGACGCCCTGAGTCCGCTCGGAGCGCGGCTCGAAGAC 135
 Qy 379 CGCTCGTGTCTTTCAGGCGCGGCTTGTGCTGAAAGAGAGCTGATGTTGTTCAACAGC 438
 Db 136 AGGTGTCTGCGGTGTCTGAGCCCGCAGAGCGCTCGAAGAGAGCTGCGCTGTGTACAGC 195
 Qy 439 CTAGAAATATATGATGATGTAAGAAACCACTCATGATGAGGAGAGACTCCGTTC 498
 Db 196 CCAAGTATATATCCCTGCTCAGGAGACCCAGGTCCTAGGCAAGGAGAGCTGACAGCG 255
 Qy 499 CTAGAGACACCTTACGACATGATTTATGCTATCCGAACTCATCTGCTGCTGCTGCTG 558
 Db 256 CTGTCCGAGACATGTGAGCCGACATCTACTTCCACCCAGAGTACTTCTACTGCGCGGCTG 315
 Qy 559 GCTTCAGGCTCTGCTCCTCAGGCTGTGTGATGCGGTCTGCGGCTGAGATCCGGAATGCG 618
 Db 316 GCCGAGGGGCTGAGCTGAGCTGAGTGTGAGCTGTGCTCAGTACAGAGCTGTGCAAAATGG 375
 Qy 619 ATGGCATCATATGAGCCCTCCTGAGATCATGACCGCCAGCAAGCTTATGATGCTATTCG 678
 Db 376 CTGCGCTGTGTAGGCTCTCCCGGACCATGAGCCAGAGGCGGCTGCCAAGGCTTCTGT 435
 Qy 679 ATGTTCAACACGTTGGCTGTGAGCCGCTGATGCTCAACAGAAACCCGATCCGAGAG 738
 Db 436 GTGTTCAACAAAGTGGCCATACAGCTGACATGCCAAGCAAGAAACCGGGCTACACAGG 495
 Qy 739 GTCTTATGATGATTTGGAGTGTGACCAAGCTGCAAGAAACAGTTCACTTTCAGACAG 798
 Db 496 ATCTCTGCTGAGTGTGAGTGTGACCAATGAGCCAGAGGATCATGATCTCTTTAGAGAT 555
 Qy 799 GACCCCAAGTCTTATTTCTCCATCCAGCCCTACAGCAAGGATGATGCTTGGCCCCAC 858
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 Qy 859 CTGAAGGCTCTAATGCTGTCACACAGGTTTCGGCCAGCAAGATATACATCAAT 918
 Db 616 CTGCGAGAGTCAATGACAGACCACTGAGGCGGGGAGCAGAGGCTCTGCTGCTGCTGCT 675
 Qy 919 GTGCTTGAACACAGGAGGAGATCGGAGATGCTGATCACTTCTGCTGCTGCTGCTGCTG 978
 Db 676 CTGCTTGAACACAGGAGGAGATCGGAGATGCTGATCACTTCTGCTGCTGCTGCTGCTG 735
 Qy 979 CTGCTGAGAGTCCCTGAGTTCACGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
 Db 736 CTGCTGAGAGTCCCTGAGTTCACGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
 Qy 1039 GCCCTGCAAGGAGACCCCAAGGATGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098
 Db 796 TCAGGCATCGGGGAGACCTGAGGAGGCAATGAGGCGACAGAGTGTCTCGCCACCTC 855
 Qy 1099 ACCACCTGCTCATGAGTGTGCTGAGAGGCAAGTATCTTCTGCTGAGGCTGCTGCTGCT 1158
 Db 856 ACACAGCTGTGACAGTGTGCTGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
 Qy 1159 AACCTCGCGGCTGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1218
 Db 916 CACCTGAGTCACTGCGGAGTCACTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 975

Db 3670 CTGATGGGCTGTGGCGGCGGATGTCTGGCCCTGAGGAGGACGACGACTGAC 3729
OY 2356 TCCATCTCAGAGTCATGCTGCTCCGACATCCCTCCCTCTGGAGAC 2403
Db 3730 GCCATTGGGACGCGCTCGAAGCATGTCTTCTGCTTCTGCTGGGAAC 3777

RESULT 8
US-09-817-913-8

; Sequence 8, Application US/09817913
; Patent No. US2002061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8459
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-8

Query Match 5.3%; Score 192.4; DB 10; Length 8459;
Best Local Similarity 59.4%; Pred. No. 8.5e-48;
Matches 385; Conservative 0; Mismatches 251; Indels 12; Gaps 3;

OY 1765 CTGTGGAGGCTGTCTCTCAGAGAGGTTCTGAATGCTGTGTGTGCTCCCA 1824
Db 3133 CTGTCTTCAAGTGTGGCCAGAGAGGAGTGAATAATGCTGTGTGTGCTCCCA 3192
OY 1825 GGACACACGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1884
Db 3193 GGACACCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3252
OY 1885 GCTGTGCGCATGCGCCAGACATATCATGTGGGAGTGGCCATGCTGATGTGG 1944
Db 3253 GCAGCCAGAGCTTCTGAG---CAGAGTTGAGCGAGAGCAAGATCTCTATGAGCTGG 3309
OY 1945 GATGTCCACACAGGTAATGAGTAATGAGTAATGAGTAATGAGTAATGAGTAAT 2004
Db 3310 GACGTGACACATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3369
OY 2005 GTGTCCCTGACCGCTATGATGATGATGATGATGATGATGATGATGATGATG 2061
Db 3370 ATGTCCCTGACCGCTATGATGATGATGATGATGATGATGATGATGATGATG 3429
OY 2062 AGCAGCAGATGCGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2121
Db 3430 GTGGGACAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3489
OY 2122 CCCCGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2181
Db 3490 CCCCGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3549
OY 2182 TACGATTTAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2240
Db 3550 AGCGAGTTTGGCGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3609
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Db 3610 CCCACCCCTCTTGGGGGGCTTACAACTCTCCGCAAGATGCTTGGGTTACCTGAGAG 3669
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Db 3670 CTGATGGGCTTGGCAGTGGCGGCAATTAATCTTATCTAGAGAGAGAGAGAGAGAG 3729

OY 2356 TCCATCTCAGAGTCATGCTGCTCCGACATCCCTCCCTCTGGAGAC 2403
Db 3730 GCCATTGGGACGCGCTCGAAGCATGTCTTCTGCTTCTGCTGGGAAC 3777

RESULT 9
US-09-817-538-8

; Sequence 8, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8459
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-8

Query Match 5.3%; Score 192.4; DB 10; Length 8459;
Best Local Similarity 59.4%; Pred. No. 8.5e-48;
Matches 385; Conservative 0; Mismatches 251; Indels 12; Gaps 3;

OY 1765 CTGTGGAGGCTGTCTCTCAGAGAGGTTCTGAATGCTGTGTGTGCTCCCA 1824
Db 3133 CTGTCTTCAAGTGTGGCCAGAGAGGAGTGAATAATGCTGTGTGTGCTCCCA 3192
OY 1825 GGACACACGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1884
Db 3193 GGACACCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3252
OY 1885 GCTGTGCGCATGCGCCAGACATATCATGTGGGAGTGGCCATGCTGATGTGG 1944
Db 3253 GCAGCCAGAGCTTCTGAG---CAGAGTTGAGCGTGAAGCAAGATCTCTATGAGCTGG 3309
OY 1945 GATGTCCACACAGGTAATGAGTAATGAGTAATGAGTAATGAGTAATGAGTAAT 2004
Db 3310 GACGTGACACATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3369
OY 2005 GTGTCCCTGACCGCTATGATGATGATGATGATGATGATGATGATGATGATG 2061
Db 3370 ATGTCCCTGACCGCTATGATGATGATGATGATGATGATGATGATGATGATG 3429
OY 2062 AGCAGCAGATGCGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2121
Db 3430 GTGGGACAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3489
OY 2122 CCCCGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2181
Db 3490 CCCCGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3549
OY 2182 TACGATTTAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2240
Db 3550 AGCGAGTTTGGCGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3609
OY 2241 -----TCGCTGGGGGGGCTGCCAGGTGTACCTGAGGGTTATGCGCACCTGAC 2295
Db 3610 CCCACCCCTCTTGGGGGGCTTACAACTCTCCGCAAGATGCTTGGGTTACCTGAGAG 3669
OY 2296 CTGATGGGCTTGGCAGTGGCGGCAATTAATCTTATCTAGAGAGAGAGAGAGAGAG 2355
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Db      2825 TGACGAGCAATGATGACATTTGGCTATGAGACGCTGTGTGGCTCTAGAGAGAGAC 2884
QY      2345 ATAACCTGACATTCATCTCAGATGTCATGAGCTGCTGCATCGCTCCCTCTGAGAGA 2402
Db      2885 ATGATCTCAGACGACCATCTGTGATGATCAGAGAACGCTGTGTAATGACCTCTTAGAGAA 2942
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RESULT 14

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US-10-072-094-97
; Sequence 97, Application US/10072094
; Publication No. US2003002538A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; PRIORITY FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/238,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 97
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3183)
US-10-072-094-97
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Query Match 4.3%; Score 155.2; DB 9; Length 3186;

Best Local Similarity 54.0%; Pred. No. 1.3e-36; Matches 388; Conservative 0; Mismatches 318; Indels 12; Gaps 3;

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QY      1694 ACTTTGACTCCATCTATATCTGCCAGTACCTTCGCTGTCAGACAGCTTGCACATGCGC 1753
Db      2360 ACAGTGACACCATTTGGAATGAGCTACACCTGCTGCGTGCAGCAGCATGCTGTGGCT 2419
QY      1754 CTGCTGCGCGCTGCTGCTGAGAGCTGCTCTCAGAGAGGTTTGATGCTGCTGTGG 1813
Db      2420 GTGTCTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2479
QY      1814 TGGTCCCCCAGAGACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1873
Db      2480 TGAAGGCCCTGAGCAGCAGCTGAGAGATCCACAGCCATGAGGCTTGTCTTTTAAAT 2539
QY      1874 CTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1933
Db      2540 CAGTTGCATTAACCGC---CAATACTTGAAGACCACTAAATATAGCAAGATATTGA 2596
QY      1934 TTGTGATTTGGATGTCACACAGGTAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1993
Db      2597 TTGTGATTTGGATGTCACACAGGTAATGGAATGGAATGGAATGGAATGGAATGGAATG 2656
QY      1994 GTTGTATATATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2053
Db      2657 GCATCTGTGATCTTCACTCCATCGCTATATGAAAGGAAGCTTTTCTGCGCAGTGAG 2716
QY      2054 AGGATGCCAGCAGCAGATCGCGGCGCTGCGGCGACAGGCTTACCGCTCAAGTGGCAT 2113
Db      2717 CCCCATAATGAGTTGGAACAGCGCTTGGAGAGAGGTATGAAATATATGCTGACCCCA 2776
QY      2114 GGAAC---GGGCCCGCAGTGGTGAATGCTACTACTAGTCTGCTGCTGCTGCTGCTGCTG 2170
Db      2777 GTGGCTTGTATCTCCATCGGAGATGTTGATGATCTTGAAGCACTTACAGACCATCTGGA 2836
QY      2171 TTCCCATTTGCTGCTGAGTTTAACCCAGAAATGTGTGCTGTGCTGCTGCTGCTGCTGCTG 2230
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QY      2231 CACGGGGGGA-----TCGCTGAGGGGCTGCCAGGTGTCACCTGAGGCTTATGCCACC 2284
Db      2897 TGAAGGCGACACACCCCTCTCTTAGAGAGGTTACAAAGTACAGGCCAAATATGTTTGTCAAT 2956
QY      2285 TCACCCACTGCTGATGAGGCGCTTGGCAGTGGCGCATTTTCTTATCCATGAGAGGTGGCT 2344
Db      2957 TGACGACCAATTTGATGACATTTGCTGATGAGACGTGTGCTGCTGCTGCTGCTGCTGCTG 3016
QY      2345 ATAACCTGACATTCATCTCAGAGTCCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGAGAGA 2402
Db      3017 ATGATCTCAGACGCCATCTGTGATGATGATCAGAGAGCCTGTGTAAATGCTTCTAGAGAA 3074
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RESULT 15

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US-10-173-539-1
; Sequence 1, Application US/10173539
; Publication No. US20030059812A1
; GENERAL INFORMATION:
; APPLICANT: Richon, Victoria
; APPLICANT: Zhou, Xianbo
; APPLICANT: Rifkind, Richard A.
; APPLICANT: Marks, Paul A.
; TITLE OF INVENTION: HDAC9 Polypeptides and Polynucleotides
; FILE REFERENCE: 3254.1000-003
; CURRENT APPLICATION NUMBER: US/10/173,539
; PRIORITY FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,173
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/311,686
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/316,995
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-173-539-1
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Query Match 4.3%; Score 155.2; DB 9; Length 3186;

Best Local Similarity 54.0%; Pred. No. 1.3e-36; Matches 388; Conservative 0; Mismatches 318; Indels 12; Gaps 3;

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QY      1694 ACTTTGACTCCATCTATATCTGCCAGTACCTTCGCTGTCAGACAGCTTGCACATGCGC 1753
Db      2360 ACAGTGACACCATTTGGAATGAGCTACACCTGCTGCGTGCAGCAGCATGCTGTGGCT 2419
QY      1754 CTGCTGCGCGCTGCTGCTGAGAGCTGCTCTCAGAGAGGTTTGATGCTGCTGTGG 1813
Db      2420 GTGTCTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2479
QY      1814 TGGTCCCCCAGAGACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1873
Db      2480 TGAAGGCCCTGAGCAGCAGCTGAGAGATCCACAGCCATGAGGCTTGTCTTTTAAAT 2539
QY      1874 CTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1933
Db      2540 CAGTTGCATTAACCGC---CAATACTTGAAGACCACTAAATATAGCAAGATATTGA 2596
QY      1934 TTGTGATTTGGATGTCACACAGGTAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1993
Db      2597 TTGTGATTTGGATGTCACACAGGTAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 2656
QY      1994 GTTGTATATATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2053
Db      2657 GCATCTGTGATCTTCACTCCATCGCTATATGAAAGGAAGCTTTTCTGCGCAGTGAG 2716
QY      2054 AGGATGCCAGCAGCAGATCGCGGCGCTGCGGCGACAGGCTTACCGCTCAAGTGGCAT 2113
Db      2717 CCCCATAATGAGTTGGAACAGCGCTTGGAGAGAGGTATGAAATATATGCTGACCCCA 2776
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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(without alignments)
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Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	799.6	21.9	1155	13	BI918415
5	790.6	21.7	945	9	AL539258
6	763.6	20.9	1019	14	BM921804

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8	732.8	20.1	739	9	AU132840	AU132840
9	725.2	19.9	993	9	AL560896	AL560896
10	719.6	19.7	879	9	AL553865	AL553865
11	710.4	19.5	771	13	BI766230	BI766230
12	687.8	18.9	707	9	AU132214	AU132214
13	684	18.8	727	9	AU142214	AU142214
14	682.8	18.7	909	14	BQ962468	BQ962468
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17	650.2	17.8	842	10	BE541123	BE541123
18	644	17.7	690	10	AV653323	AV653323
19	642.8	17.6	856	12	BF528502	BF528502
20	633	17.4	633	14	BQ638151	BQ638151
21	632.6	17.3	718	12	BG819867	BG819867
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40	510	14.0	519	10	AM246112	AM246112
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LOCUS	BC013219				
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ACCESSION	BC013219.1	GI:15301482			
VERSION	BC013219.1				
KEYWORDS	HTC.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1688)				
TITLE	Strausberg, R.				
JOURNAL	Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				

REMARK COMMENT
Contact: MGC help desk
Email: cga@bbs.femail.nih.gov

Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLU)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalob@bcm.tmc.edu

301 TGGATGACAGCTTCCCGAGAGGCGCTGAGGCTCCATCCATCAAGAGCACTATC 360
318 TGGATGACAGCTTCCCGAGAGGCGCTGAGGCTCCATCCATCAAGAGCACTATC 377
361 CAGAGAGGCGCTTCTAGATGCTGCTGCTTCCAGGCGCGCTTCTGAGAGAGAG 420
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601 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
618 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
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798 ACAGTTCACCTTCCGAGAGGCTGCTTATGATGATGATGATGATGATGATGATGAT 857
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900 CCAAG 904
917 CMAAG 921

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DEFINITION 603176195F1 NIH_MGC_121 Homo sapiens cDNA IMAGE:5240639 5',
mRNA sequence.
ACCESSION B1918415
VERSION B1918415.1 GI:16182107
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1155)
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1606 row: m column: 24
High quality sequence start: 29

High quality sequence stop: 825.
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5240639"
/clone_1id="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site: 1: Notii;
Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3
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and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH-MGC Library."

BASE COUNT 294 a 315 c 348 g 198 t
ORIGIN

Query Match 21.9%; Score 799.6; DB 13; Length 1155;
Best Local Similarity 97.8%; Pred. No. 1.3e-194;
Matches 843; Conservative 0; Mismatches 14; Indels 5; Gaps 3;

2498 GCTTACGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2557
32 GCTTACGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 91
2558 AGAAGGACACCCCAACACCAACCTAGTATGATGATGATGATGATGATGATGATGAT 2617
92 AGAAGGACACCCCAACACCAACCTAGTATGATGATGATGATGATGATGATGATGAT 151
2618 AGTTCTGAG 2677
152 AGTTCTGAG 211
2678 CAGGCGCAGTACTGAG 2737
212 CAGGCGCAGTACTGAG 271
2738 CAGGCGCAGTACTGAG 2797
272 CAGGCGCAGTACTGAG 331
2798 TGGTGGGACAGACCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2857
332 TGGTGGGACAGACCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 391
2858 CAG 2917
392 CAG 451
2918 GAGCCAGGCTGGGACAGACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2977
452 GAGCCAGGCTGGGACAGACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 511
2978 CCATCTCGAG 3037
512 CCATCTCGAG 571
3038 CAGGCGCAGTACTGAG 3097
572 CAGGCGCAGTACTGAG 631
3098 CAACCTCAGCTTGGAG 3157
632 CAACCTCAGCTTGGAG 691
3158 TGAAGACCTTGGAG 3217
692 TGAAGACCTTGGAG 751

[illegible][illegible]

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/db_xref="taxon:9606"
/clone="IMAGE:5753394"
/lab_host="DH10B"
/Note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site: 1; NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

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BASE COUNT 248 a 278 c 290 g 198 t 5 others

Query Match 20.9%; Score 763.6; DB 14; Length 1019;
 Best Local Similarity 98.5%; Pred. No. 2.2e-185;
 Matches 781; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

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OY 1 ATGACCTCAACCGGCGAGATTCACACCAACGAGGAGAGTAGGAGACCC 60
DB 91 ATGACCTCAACCGGCGAGATTCACACCAACGAGGAGAGTAGGAGACCC 150
OY 61 CAGTGGCCCTCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 151 CAGTGGCCCTCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 210
OY 121 CCCCCCTCTATCCCAATCTAGCGAGGTAAGAAAGGCAAAATGAGAACTCG 180
DB 211 CCCCCCTCTATCCCAATCTAGCGAGGTAAGAAAGGCAAAATGAGAACTCG 270
OY 181 CAAGCAATGAGAGAGAGCTATATGCTGAGTGCAGAGGAGTGTACCTTACGCT 240
DB 271 CAAGCAATGAGAGAGAGCTATATGCTGAGTGCAGAGGAGTGTACCTTACGCT 330
OY 241 GAAGCACTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 331 GAAGCACTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 390
OY 301 TGGGATGACAGCTTCCGGAAGGCGCTGAGGCGCTGCTGCTGCTGCTGCTGCT 360
DB 391 TGGGATGACAGCTTCCGGAAGGCGCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCT 450
OY 361 CAGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 451 CAGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 510
OY 421 CTGATGTTGGTTCACAGCTAGATATATATGATGATGATGATGATGATGAT 480
DB 511 CTGATGTTGGTTCACAGCTAGATATATATGATGATGATGATGATGATGAT 570
OY 481 GAGGAGAACTCGGTGCTAGACAGACCTGACACTGATTTATCTGATCCGAACTCA 540
DB 571 GAGGAGAACTCGGTGCTAGACAGACCTGACACTGATTTATCTGATCCGAACTCA 630
OY 541 TACTCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 631 TACTCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
OY 601 GGTGAGATCCGGAATGGCATGGCATATAGGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 691 GGTGAGATCCGGAATGGCATGGCATATAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 750
OY 661 CTTATGATGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 751 CTTATGATGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 810
OY 721 AAACACCGATCCGGAAGGCTCTTATGATGATGATGATGATGATGATGATGAT 778
DB 811 AAACACCGATCCGGAAGGCTCTTATGATGATGATGATGATGATGATGATGAT 870

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OY 779 CACAGTTCACCTT 791
 DB 871 CACAGTTCACCTT 883

RESULT 7
 LOCUS A0132867
 DEFINITION A0132867 NT2RP4 Homo sapiens CDNA clone NT2RP4000749 5', mRNA
 ACCESSION A0132867
 VERSION A0132867.1 GI:10993406
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 807)
 AUTHORS Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
 Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
 Isogai,T.
 HRI human CDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
 Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano
 S., Masuho,Y., Isogai,T.)
 JOURNAL Unpublished (2000)
 COMMENT Contract: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; CDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 FEATURES
 source Location/Qualifiers
 1. 807
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="NT2RP4000749"
 /clone_lib="NT2RP4"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /note="Vector: pME18SFL3; mRNA from NF2 neuronal precursor
 cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT 171 a 238 c 215 g 179 t 4 others

Query Match 20.7%; Score 756; DB 9; Length 807;
 Best Local Similarity 98.0%; Pred. No. 1.8e-183;
 Matches 785; Conservative 0; Mismatches 13; Indels 3; Gaps 2;

```

OY 292 CATTGCGCTGGGATGACAGCTCCGGAAGGCGCTGAGGCGCTGCTGCTGCTGCTGCT 351
DB 1 CATTGCGCTGGGATGACAGCTCCGGAAGGCGCTGAGGCGCTGCTGCTGCTGCTGCT 60
OY 352 CAACATGATCCAGAGAGGCGCTCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
DB 61 CAACATGATCCAGAGAGGCGCTCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
OY 412 AAGGAGAGCTGATGTTGTTGCTGACAGCCGTAAGTAATATGATGATGATGATGAT 471
DB 121 AAGGAGAGCTGATGTTGTTGCTGACAGCCGTAAGTAATATGATGATGATGATGAT 180
OY 472 TACATGATGAGGAGGAGAACTCCGCTGCTAGACAGACCTGACACTGATTTATCTGAT 531
DB 181 TACATGATGAGGAGGAGAACTCCGCTGCTAGACAGACCTGACACTGATTTATCTGAT 240
OY 532 CCGAATCATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
DB 241 CCGAATCATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

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SOURCE

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Li, W. B., Gruber, C., Jesse, J. and Polayes, D.	Full-length cDNA libraries and normalization	unpublished (2001)	Contact: Genoscope

FEATURES

Location/Qualifiers
1. .993

BASE COUNT	202 a	258 c	297 g	234 t	2 others
ORIGIN					

QY	2917	GGAGCCACGCTGGGGCCAGACTACTCTAGAGGAGGCTGTAGAGAGAGCTACACTGGCCAG	2976
Db	993	GGAGCCACGCTGGGGCCAGACTACTCTAGAGGAGGCTGTAGAGAGAGCTACACTGGCCAG	934
QY	2977	ACCATCTCGAGAGGAGCCATGAGGAGGAGCCACACTGGACACAGTACTGCTCAGAGGAGCT	3038
Db	933	ACCACCTCGAGAGGAGCCATGAGGAGGAGCCACACTGGACCCAGMTACTCTCAGAGGAGCT	874
QY	3037	CCAGGGGGCCACGAGCTGATCCAAACTCTCTAGCCTCGAGACAGACACACAGACCCCC	3098
Db	873	CCAGGGGGCCACGAGCTGATCCAAACTCTCTAGCCTCGAGACAGACACACAGACCCCC	814
QY	3097	CCAACTCACCCTGTCGACAGGAACTACACCCAGATATCTCCAGTACACTGATTTGGAGT	3156
Db	813	CCAACTCACCCTGTCGACAGGAACTACACCCAGATATCTCCAGTACACTGATTTGGAGT	754
QY	3157	CTCAGGACCTTGGAGCTAGGACGAGGAATCTCAGGGGGCTCAGAAATCCAGGCCCCAGGA	3216
Db	753	CTCAGGACCTTGGAGCTAGGACGAGGAATCTCAGGGGGCTCAGAAATCCAGGCCCCAGGA	694
QY	3217	GAGGAGAACCTTACTAGGAGAGGAGCGAGCTGAGAGTACAGCATATGGTGATTCAGTCTGATG	3276
Db	693	GAGGAGAACCTTACTAGGAGAGGAGCGAGAGTACAGGACATGGCTGATTCAGTCTGATG	634
QY	3277	CAGGAGCTAGGGGGCTCACTGATCAGGCCATATTTATGCTGTGACACCACTGCCCTGG	3336
Db	633	CAGGAGCTAGGGGGCTCACTGATCAGGCCATATTTATGCTGTGACACCACTGCCCTGG	574
QY	3337	TGTGCCCATTTGGTGGGAGATGTGCCCATATCTGACAGAGGCTTAGAGAGTGAACCAACT	3396
Db	573	TGTGCCCATTTGGTGGGAGATGTGCCCATATCTGACAGAGGCTTAGAGAGTGAACCAACT	514
QY	3397	TGTGGGGAGCTGTGAAACAATCCAGAGAAATTTGGGTGTGCTCTCTGCTAACAAGGTAC	3456
Db	513	TGTGGGGAGCTGTGAAACAATCCAGAGAAATTTGGGTGTGCTCTCTGCTAACAAGGTAC	454

QY	3457	TGTGGTGGTACATCAATATGGCCACATCTCTCCAAACACATATGGAATTTGTGGACACCCGCT	3510
Db	453	TGTGGTGGTACATCAATATGGCCACATCTCTCCAAACACATATGGAATTTGTGGACACCCGCTG	394
QY	3517	GTCTCTCAGTACATCGACCTGTCTCAGCCTGGTGTACTACTGTCTCAGGCCCTATATGCCACAC	3576
Db	393	GTCTCTCAGTACATCGACCTGTCTCAGCCTGGTGTACTACTGTCTCAGGCCCTATATGCCACAC	334
QY	3577	CAGGCTCTCTAGATGTGGAAGAACATCGCCACACGAGAACAAATTTGGGAGAGATATGCC	3636
Db	333	CAGGCTCTCTAGATGTGGAAGAACATCGCCACACGAGAACAAATTTGGGAGAGATATGCC	274
QY	3637	CACCCACACTTA 3648	
Db	273	CACCCACACTTA 262	

RESULT 10	
AL553865	
LOCUS	879 bp mRNA
DEFINITION	Al553865 LTT-NFL006-P12 Homo sapiens CDNA clone CS01077YH01 5
ACCESSION	prime, mRNA sequence.
VERSION	AL553865
KEYWORDS	AL553865.1 GI:12894100
SOURCE	EST.
ORGANISM	human.
	Homo sapiens

REFERENCE 1 (bases 1 to 879)
AUTHORS I.A.W.B., Gruber,C., Jesse,J. and Polyes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
FEATURES
source I..879

	BASE COUNT	218 a	237 c	243 g	178 t	1 others
ORIGIN						
Query Match	19.7%;	Score 719.6;	DB 9;	Length 879;		
Best Local Similarity	98.3%;	Prd. No. 4.5e-174;				
Matches 769;	Conservative 0;	Mismatches 9;	Indels 4;	Gaps 4;		
QY 1	ATGACCTCAACCGGCCAGATTCGCCACCAACCGCAGCGAGCGAAGAAAGTAGGCGCAACCCC	60				
Db 65	ATGACCTCAACCGGCCAGATTCGCCACCAACCGCAGCGAGCGAAGAAAGTAGGCGCAACCCC	124				
QY 61	CAGTCGCCCCCTCAGGACTCTCAAGTCTCACTTCGAAAGGAAATATTTAAANAAGGAGCCGTT	120				
Db 125	CAGTCGCCCCCTCAGGAGCTCAAGTCTCACTTCGAAAGGAAATATTTAAANAAGGAGCCGTT	184				
QY 121	CCCCGCTCATCCCAATCTAGGGGAGGTAAANAAGGCAAAATGAGAGAGCTCGGC	180				
Db 185	CCCCGCTCATCCCAATCTAGGGGAGGTAAANAAGGCAAAATGAGAGAGCTCGGC	244				

FEATURES	LOCATION/Qualifiers	row	g	column	stop	771
DB	101 CMGCAATGGAAGAACCTTAATCTGGGCTCTCCAAAGCAAGCATCTGAAACCTTGAGAGCT	240				
DB	245 CAAGCAATGGAGAGAACCTTAATCTGGGCTCTCCAAAGCAAGCATCTGAAACCTTGAGAGCT	304				
DB	241 GAAGCACTGGCTGGCACTGGCTTGGTGGATGAGACAGTTAAATGATTCATTCGCTC	300				
DB	305 GAAGCACTGGCTGGCACTGGCTTGGTGGATGAGACAGTTAAATGATTCATTCGCTC	364				
DB	301 TGGAGTGAACGCTTCCCGGAGAGGCCCTGAGCGGCTCCATGCCATCAAGAGCAACTGATC	360				
DB	365 TGGAGTGAACGCTTCCCGGAGAGGCCCTGAGCGGCTCCATGCCATCAAGAGCAACTGATC	424				
DB	361 CAGAGAGGCGCTCTAGATGCGTGGCGTCTTCAAG-GGCCGGTTGCGTGAAG-GAAG	418				
DB	425 CAGAGAGGCGCTCTAGATGCGTGGCGTCTTCAAGGCCGGTTGCGTGAAGAGAG	484				
DB	419 AGCTGATGTTGGTTCCACAGCTTAGAATATATGATGTGATGAGAAACACCGAGTACATGA	478				
DB	485 AGCTGATGTTGGTTCCACAGCTTAGAATATATGATGTGATGAGAAACACCGAGTACATGA	544				
DB	479 ATGAGAGGAGAACTCCGTGCTCTAGACAGACACTACACTCACTTATCTGCATCCGAACT	538				
DB	545 ATGAGAGGAGAACTCCGTGCTCTAGACAGACACTACACTCACTTATCTGCATCCGAACT	604				
DB	539 CATACTCTGTGCGCTGAGGCTGAGGCTCTGTCTCTCAGGCTGGTGGATGCGGTCTGG	598				
DB	605 CATACTCTGTGCGCTGAGGCTGAGGCTCTGTCTCTCAGGCTGGTGGATGCGGTCTGG	664				
DB	589 GGGCTGAGATCCGGAATGGCATGSCCATATTAGGCGCTCTGAGCATACGCCAGACCA	658				
DB	665 GGGCTGAGATCCGGAATGGCATGSCCATATTAGGCGCTCTGAGCATACGCCAGACCA	723				
DB	659 GTCCTATGAGATGGGCTATGTCATGTCATCAACACAGTGGCTGTGGCAAGCCGCTATGCTCAAC	718				
DB	724 GTCCTATGAGATGGGCTATGTCATGTCATCAACACAGTGGCTGTGGCAAGCCGCTATGCTCAAC	782				
DB	719 AGAAACACCCGATCCGGAGAGGCTCTTATGATGATGGATGGATGGACACAGGTCAGAGAA	778				
DB	783 AGAAACACCCGATCCGGAGAGGCTCTTATGATGATGGATGGATGGACACAGGTCAGAGAA	842				
DB	779 CA 780					
DB	843 CA 844					
RESULT 11						
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DEFINITION	603052876p1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5202475 5',					
ACCESSION	B1766230					
VERSION	B1766230.1					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
TITLE	1 (bases 1 to 771)					
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.					
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)					
	Unpublished (1999)					
	Contact: Robert Strausberg, Ph.D.					
	Email: cgabds-remail.nih.gov					
	Tissue Procurement: Life Technologies, Inc.					
	cDNA Library Preparation: Life Technologies, Inc.					
	CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN)					
	DNA Sequencing by: Incyte Genomics, Inc.					
	Clone Distribution: MGC clone distribution information can be					
	found through the I.M.A.G.E. Consortium/LNLN at:					
	plate: LRAM1507 row: g column: 20					
	High quality sequence stop: 771.					
	Location/Qualifiers					

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1. 771
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/db_xref="taxon:9606"
/clone="IMAGE:5202475"
/clone_1ib="NIH.MGC_122"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pcMV-SpOst6
Site.1: NotI; Site.2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note
this is a NIH.MGC Library."

BASE COUNT      193 a      243 c      219 g      116 t
ORIGIN

Query Match      19.5%; Score 710.4; DB 13; Length 771;
Best Local Similarity 97.5%; Pred. No. 1e-171;
Matches 753; Conservative 0; Mismatches 16; Indels 3; Gaps 3,

QY      2327  TTATCTAGAGGGGTGGCTATTAACCTGACATCTCAGAGTCAGATGCTGCTGCACTC 2386
D      1  TTATCTAGAGGGGTGGCTATTAACCTGACATCTCAGATCTCAGATGCTGCTGCACTC 60
QY      2387  GCTCCCTCTTGGAGAGCCACACACCCCGGCGAGACCTGCGACGCGCCCGCCACTATCAAGGG 2448
D      61  GCTCCCTCTTGGAGAGCCACACACCCCGGCGAGACCTGCGACGCGCCCGCCACTATCAAGGTG 120
QY      2447  CCTGGCCTCATCTAGACACATTCACAGTCACGAGATCTGCGAGTTCAGTTCACGG 2508
D      121  CCTGGCCTCATCTAGACACATTCACAGTCACGAGATCTGCGAGTTCAGTTCAGTTCACGG 180
QY      2507  TCATGAGGTGAAAGACAGAGAGAGACCTCCAGTTCTTAAGTTGGTCCACAAGAGGCAC 2566
D      181  TCATGAGGTGAAAGACAGAGAGAGACCTCCAGTTCTTAAGTTGGTCCACAAGAGGCAC 240
QY      2567  CCCAACCCGCAAAACCTAGGTTACTGAGGGGAGAGACACACGAGAAAGAAAGTTCTCG 2626
D      241  CCCAACCCGCAAAACCTAGGTTACTGAGGGGAGAGACACACGAGAAAGAAAGTTCTCG 300
QY      2627  AAGCAGGCGATGGGAAAGTCACTCTGCGCATCTATTGGGGGAAGAGTCCACTCCAGCCAGA 2686
D      301  AAGCAGGCGATGGGAAAGTCACTCTGCGCATCTATTGGGGGAAGAGTCCACTCCAGCCAGA 360
QY      2687  CTAATCTAGAGACAGCTGTGTGGTGGCCCTCACTACAGACCAAGCCTCTCAGAGCCACAG 2746
D      361  CTAATCTAGAGACAGCTGTGTGGTGGCCCTCACTACAGACCAAGCCTCTCAGAGCCACAG 420
QY      2747  GGGGAGCCACCTCTGGCCACACACTTTCGAGGAGAGCATTTGGGGGAGCCATGCTGGGCC 2806
D      421  GGGGAGCCACCTCTGGCCACACACTTTCGAGGAGAGCATTTGGGGGAGCCATGCTGGGCC 480
QY      2807  AGACCACTCAGAGAGAGGCTGTCTGGGGAGACCACTCCGACCAAGACCACTCAGAGAGAGA 2866
D      481  AGACCACTCAGAGAGAGGCTGTCTGGGGAGACCACTCCGACCAAGACCACTCAGAGAGAGA 539
QY      2867  CTGTGGGAGAGAGCCATTCTGGACCAAGACCACTTCAGAGATGTCTGTTGGGGAGCCACGC 2926
D      540  CTGTGGGAGAGAGCCATTCTGGACCAAGACCACTTCAGAGATGTCTGTTGGGGAGCCACGC 599
QY      2927  TGGGCCAGACTACCTCAGAGAGGCTGTAGAGAGAGTAC-ACGCGCCAGAGACATCTCG 2985
D      600  TGGGCCAGACTACCTCAGAGAGGCTGTAGAGAGAGTAC-ACGCGCCAGAGACATCTCG 659
QY      2986  GAGGACACCATGGAGGAGGACCACTAGACCACTAGCTCAGAGAGAGGCTCCAGAGGGGC 3045
D      660  GAGGACACCATGGAGGAGGACCACTAGACCACTAGCTCAGAGAGAGGCTCCA-GGGGC 718
QY      3046  ACCGAGTGTATCCAAACTCTCTTAGCCTGAGACACAGACCAACCCGCC 3097

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Db 719 ACCGAGTGAATCCATCTCTAGCCTCCACAGACAGACAGAACCCCCC 770

RESULT 12
LOCUS AU132214
DEFINITION AU132214 NT2RP3 Homo sapiens cDNA clone NT2RP3004011 5', mRNA
ACCESSION AU132214
VERSION AU132214.1 GI:10992568
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 707)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. 707
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/db_xref="taxon:9606"
/clone="NT2RP3004011"
/clone_lib="NT2RP3"
/cell_type="teratocarcinoma"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT 125 a 204 c 203 g 170 t 5 others
ORIGIN

Query Match 18.9%; Score 687.8; DB 9; Length 707;
Best Local Similarity 98.9%; Pred. No. 6.4e-166;
Matches 700; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1657 AAAATGAAACCCGGAGCTGCACCGTAGAGTTCACACTTGACATCATATATCGC 1716
DB 1 AAAATGAAACCCGGAGCTGCACCGTAGAGTTCACACTTGACATCATATATCGC 60
QY 1717 CCGACTACCTTGGCCCTGTGCACAGCTTGCACATGCGCCCTCCCTGCTGGAGGCT 1776
DB 61 CCGACTACCTTGGCCCTGTGCACAGCTTGCACATGCGCCCTCCCTGCTGGAGGCT 120
QY 1777 GTGCTCTGAGAGAGTTCGAATGCTGCTGTGTGCTGCTGCCGCCAGACACACGCA 1836
DB 121 GTGCTCTGAGAGAGTTCGAATGCTGCTGTGTGCTGCTGCCGCCAGACACACGCA 180
QY 1837 GAGCAGATGAGAGCTTGGCTTTTTCCTTTTCACTCTGCTGCTGCTGCTGCTGCTG 1896
DB 181 GAGCAGATGAGAGCTTGGCTTTTTCCTTTTCACTCTGCTGCTGCTGCTGCTGCTG 239
QY 1897 GCCCAGATATCATGCTGGGATGCCCTACAGGATCCTGATTTGGATTTGGATTTGGATTT 1956
DB 240 GCCCAGATATCATGCTGGGATGCCCTACAGGATCCTGATTTGGATTTGGATTTGGATTT 299
QY 1957 GGTATGGAATCTACACATGTTTGGAGATGACCCAGTGTGCTATATATGTGCTCCCTGAC 2016
DB 300 GGTATGGAATCTACACATGTTTGGAGATGACCCAGTGTGCTATATATGTGCTCCCTGAC 359

QY 2017 CGCTATGATCATGGACACTTCTTCCCATGCGGGATGAGGGTGCACAGCCAGATCGGC 2076
DB 360 CGCTATGATCATGGACACTTCTTCCCATGCGGGATGAGGGTGCACAGCCAGATCGGC 419
QY 2077 CGGGCTCGCGGCGACAGGCTTACCCGTCACAGTGGCATGGAACGGGCCCCGATGGGTAT 2136
DB 420 CGGGCTCGCGGCGACAGGCTTACCCGTCACAGTGGCATGGAACGGGCCCCGATGGGTAT 479
QY 2137 GCTGACTACCTACCTGCTGCTGCGATCGGATCGGCTGCTGCTGCTGCTGCTGCTGCT 2196
DB 480 GCTGACTACCTACCTGCTGCTGCGATCGGATCGGCTGCTGCTGCTGCTGCTGCTGCT 539
QY 2197 GAACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2256
DB 540 GAACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
QY 2257 CAGGTGTACCTGAGGAGGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2316
DB 600 CAGGTGTACCTGAGGAGGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 659
QY 2317 GCGATTATCTTATCTTATAGAGGCTGCTATACCTGATCCATCCATCTCA 2364
DB 660 GCGATTATCTTATCTTATAGAGGCTGCTATACCTGATCCATCCATCTCA 707

RESULT 13
LOCUS AU142214
DEFINITION AU142214 VESENI Homo sapiens cDNA clone VESENI000472 5', mRNA
ACCESSION AU142214
VERSION AU142214.1 GI:11003735
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 727)
Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T.,
Nishikawa,T., Nakamura,Y., Sugano,S., Masuno,Y. and Isogai,T.
HRI human cDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S.,
Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S.,
Masuno,Y., Isogai,T.)
TITLE Unpublished (2000)
JOURNAL Contact: Takao Isogai
COMMENT Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. 727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="VESENI000472"
/clone_lib="VESENI"
/cell_type="umbilical vein endothelial cell (HUVEC)"
/note="Vector: pME18SFL3; primary endothelial cells"
BASE COUNT 140 a 221 c 214 g 149 t 3 others
ORIGIN

Query Match 18.8%; Score 684; DB 9; Length 727;
Best Local Similarity 98.9%; Pred. No. 6.1e-165;
Matches 698; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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DB 1 AACACGAGGCTGGGAGCCCGGATGCTCAACAGAAACACCGCATCCGGAGGTCCTT 60

